

901

TTTCCTTATT AATACTTCAG CTCCTTAAC CTCTACTTT TCAACTTAAG GGTACTTGCT	120
TGAGATGGTC TGAAACACTG TGTTTGAAAG GGAAGGCATC CAGAATTAAA TTTTAGTTAC	180
TTAAAAATTT ATTTCTCAAA GTCTCTCTCA ATCTTGTCCTC TTACTCTTTG ACATCCAGAA	240
ATGAGTAGTT TTCCAACAAT GGTACATCCA ATATCTGGAC TCCCTTTATT GTCTTTTATT	300
GGTTGCTAAC AATATGTGGA TGATTGCTTA TGCTCATCTA TTTTTT TAGA ATATTCATTT	360
ATnATTTAAA AGACAGAGGT GCAGAGAGGC AGAGGGCAGA GAGAAAGAGA AAAGGGGGGA	420
GGGTTCTTCA TCTGCTGGTn CACTCCCCAG ATGTCCGCAA TGGCCAGAGC GTGCCAATCC	480
GAAGCCAGGA GCCAGGATCT CTCGGGnCTC CCAnGTTGAT GCAGAnGCCC AAGAACTGGG	540
GTAnCTTCTA CAGATTCTCTC AGGCCTAGAA GACAGCGGGA TGAGAA nTGG AGCAGCCGGG	600
ACTAGAACCA GCGCCCAAAT GGGGATTCTG GGCCTGCAG GCGGCAGCTT TACCTG	656

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

AGCTGAATCT TCAAATTCAC AGAAATTATG ACTTACAAAG TCATCACACA CTGAATTAGC	60
AAATACAGAG ACTCTGTCCC TAGTGGGAAT ACAGGATCAG GTGCCTATGA GCCTCTGGTC	120
AAAATATTCT CAAAAACAAT CAGCAAAGAT CCTGTCTAAA GAAACCTCAT TCAATATACT	180
GTGTTGCATC ACTGAACTCA TAGCCAGTAG CTCCTTTT TA AATTTATTTT TTAGATTAT	240
TTATTTGAAA GTCAGAGTTA CAAAGAGAGA GGGAGACATA GAGATCTTCC ATCTGCCAGT	300
TCACCTCTCC AATAGCCACA ACAGCCAGGG TTGGGCCAGT CTGATGCCAG GAGCCTAGAA	360
CTCCATTCAA GCCTCCCACA TGGGTACAGG AGCCCAAGGA CTTGAGCCAT CCTCTGCTGC	420
CTCCAGGTT CC	432

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TGATGCCTGC ATTATAATTA AATAATGCCT ATCACCGTTT CTTAAGCAAC AAATGATCAC	60
AGATTCCCTC TTTGCTGCTA AGTAATGAGC ATGGTGATTC TTCCCTCCGT AACCACCTCC	120
CCACCTACAC TCCCTCCCCT CTCCTCCTT CCTCTCCTAT TGACATGGAG TGCCATACAT	180
AGCTAGGGTG AACATTTATC CCGCTTGGCC CTAGGTGTTT ATACACTTCA ACTGTGTGTA	240
ATTATTTCATA TGCCCTTTTT ATGACCAAGC TTATGTCAGA ACGACAAATT ATATATTAC	300
CTAATACTGA GAATCATCAA ATTGATTTCT ATTTTCTTCT CTCTTAGGCA GTTCTTGAGG	360
GGCAGAAATA TTTATTTTGT ATATCATGTA TTTATTCAAC TAAAAGACTG ACTGTCAAGA	420
TGCTGAGTTT TAGTGTCAAA GCAAATATGT TTCTAGACCC CATGAAGTTT ACAGTCTGGC	480
AAGAAAGAGC CATCTACCCC AAGAATATTG TTTAACATAG TAAATGCTGG TGTGAAGTCA	540
GTGGATAAAA ATTGAAGCAT TCTTAATCTA GC	572

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

AAAAGGAATA AAAGAAAAA CCAACACACA CACACACACA CACACACACA ACTGTTGAAG	60
GAAGCTCTCT TTGCTCTCAC TCTCACTGTG CCTTTCAAAT AGATGTGAGA AAAAATGTGA	120
AAGAGGGAAA CAGAAAAGTA GGACACAGAG ATATGACACG AGATGGACTG GACCTGCCAC	180
TGCTGTCTCT GAAGATGAAG GCAAGGGCCA TATGGTGGCA TCTCAAAGCT GGGAAGTACC	240
CTCAGCTGAC AGCCTATAGG AACAGGGAC TTGAAACGAA AACTGATTTT GGCATTGTGA	300
AGTTAATTAT TACTGTTAAC AACTACCTAA AAATATGAAG GGGCTGCATT GTGTGAAGCA	360
GGTAAACCA CTGCTTGAGA TGCTGACACT TCATATAGGA GTGCTGGTTC AAGTCCCTGC	420
TACTCCACTT CCAATCTAAC ACCTTGCTAA TGCACCTGGG AAAGTAGTGG ATGATGGCTT	480
AAGAACTTGG GCCCCTGCAA CCCATGGAAG AGACCAGGAT GCnGTTCCAG TTTCTTGGCT	540
TTGTCTGAC CCAGnCCCAG CCATTGTGGC CAT	573

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

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CAGTTTGTGA TAAGACAGCA ATGTGTAAAG CATATTCCTT TGA CT CAGCA GCACTTGCCA      60
CTCAATTTTC TCAACAGTTT GTGTAATAAT ACAATTATTG TTGTTATTAA TATTTTATT      120
AAATTCACC AATAAATGCC TTAGTTGCAT CATCTTATTT CTTATTAAAA AGCTTTTTTT      180
AAAAAAGTT TATTTATATT TATTTGAAAA GCACAGAGAG AGAGAGACAG AGAGATATTC      240
CATCAGTTGA CTCACTCCTC AAATGCCTGC AACAGCTGGG GCTGGGCCAG GACAAAGCCA      300
GGAACCAGGA GTCAGGA ACT TCATGTGGCA GAGACCCATG TCCTTGGGTG ATCATTAGCT      360
ACTTTCAGT GTGCACTTTA ACAGGAAGTT GGATCAAAAG TAGAGCCAAG GTTTGAGCCT      420
GGCACTTGAT CTGGGATACA GGTATCCCAG GCAGCGACTT GGACCACTCC TCCAAATGAC      480
CATACCCCAT TTGTACCAAC TCAGAGTGGT TCATGAATAG GCTGAAAGAG AGAACAGCTG      540
TTTAGTGCCT TACATATTTT CATCAAGGAA TACTTTTTTT GGTCTCTTGG GATGAACATG      600
GAA                                                                                   603
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(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 614 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

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CAATGGGTnC AACCCAAGCC AGACCCCTGA AGGCCACTCA GAACAACAGG CTTGGGAGCC      60
AGTGTGTGG TACAGCAGGT TAAGCTGCCG CCTATGATGC CAGCATCCCA TGTGAGTCCC      120
TGTTCAAGTC CCGGTGCTCC ACGTCCAATT CAGCTGCCTG CTAATGCACA AAAGAAAGTA      180
GCAGCAGATG GTCCGTGTGC TTGGGTCCCT GCACCCACAT GTGAGACCCA GACGGAGTTC      240
CAGGTTCTTG GGTTCACCC AGCCTAGCCT CAGCTAGGTA GCCATGTGGG GAAGTGAACC      300
AGTAGATGGA AACCAGCTCG CTCTCTGTCT TTCCCTTTCT CTAATTCTGT CTTTCAAAGA      360
AATAAACAAA CAAATTTGGA AAAACACCTC ACTGGACTGA TAGCACCTGA GTCCCTCCCT      420
CTGCAGCCCA TGCCCCAGTG TACACTCCTC AAGACACCGG CATGCACCTG CCTAGCCCCT      480
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CCACAAGGCA TTATCAGGGC CCCTCCAGT GTTTCCTCTT CGATCCCAAG GnTCGAAGGG 540
ATTGAATCCC CAGGATTTGn GCCGGCGCTG CGGCTCACTA GGnTAATCCT CCGCCTAnAG 600
GCGCCGGGGA AAAn 614

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

CCAGACCGGA AGGAAGGAGT ACGAATGTTA TTGAGTGTGG AAACGATAGT GCAGATTTAC 60
TTCAAATAC ACCAGCAGGG GCAGGTGCTG TGGTGGCGCA GGTTAGGCCA CAGCTTGAGA 120
AACCCACATC CCGTATCAGA GTGCTGGTTC GGATCCCGGC TGCTCCAGCA TTCCTGCTAC 180
TGCGCCTGGG AGGCAGCGGA TCAGGACCCA GGTACTCGGG TCCTGCCACC CACGTGGGAG 240
ACCCAGATGC AGCTCTTGGC TCCTGACGTA GCCTGGCCTA GTCTTCTGT TACAGGCATT 300
TGAGAAACAA ACCAGCAGAT GGCAGATCTC TCTCTCTGGC CTCTCTCCCT CTCACTCTCT 360
CTGTTGTTCT GCCTTTCCAG TAAATAAATA AATCTTTAAA AAGATAAATA AAGTACCCCA 420
GTAAAGCAA CCACATAACT TCTACACAGA AATGAGCAGA TGTATCAGGA CATTAAAGAA 480
AGCATAAATG AATAGAAAGA TGTA 504

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

TTTTTGAGAA CTCTTAATG TTCTTATCAA TTTTTTGAGA TCTGCTTCTT GCATTTCTTC 60
TATGTCATCA TCTTCATAAT CTTGAATTGG GGTGTCTTTT TCATTTGAGG GCGTCATGGT 120
GACTTCCTTG TTTTATTAC CTCGGTTTTT GCGTTTGTTA TTGGCATAT TGGAGATATT 180
TGGTTTCTTC ACTGTGGTGC TTTTCTTGT TATACTATGA CTCTAGATTA AGTGGACTAT 240
CTGTTTTTGA TGGAGCCTTA GGGCTTGAGA TGGGTGTGGC CTGAGAGCTC TGTTGGTGT 300

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GCCAAAGGTG ACACTCCCAG GTTAGGCGTG GTAAATCTCT CTCTCTCTCT CTTTTTTTTT 360
TTTGATTCAA AAGGGAAGTA ATTCCGCACA GCTGAACGAA GTGGAGGTAG TTAG 414

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CTGATTTGAG TATTGGTCAT ATTCTTGAAA GACACAATCC TGAAAGCCAT CTACCCAAAC 60
ATTAGAATTC CAAAAGATCA AAATCTACTA TCTAAAGAAT CACAACCCGA AAATTAAAAT 120
CCTTAATTTT GAAAACCTGA AAGCCAAAAT CCCCAAACT TATTGCCTGT TTTTTTTTTT 180
TTAAGAGAAT CACTTTCTAA AACTTATTAA GTATTTATTT GAAAGGCAGA ATGACCAAGA 240
GAGAAGGAAA AACAGAGAGA ATGAGCTTCC ATCTGCTGGT TCACTTCTCA CATGGTCACA 300
ACAGGGAAGG GCTGGGCCAA AGAAAGGAAC TCCATCCAAG TCTCCACAT GGGTGGACAG 360
GGACCCAATT ACCTGGAATC ATTCCTGGC TGGCCTTCCA GGTGGCATTG GCAGGAACT 420
GGATAGGAAG TGGAGTAGCT GAGACTCAAC CAGTGGCTCC GATATATGAT GGCGGTGTCA 480
CAGGGCAGCT TAACCTGCTG TACCACAACA CCTGAACCAG TAAATGTCAT GTTTTTTAAA 540
AAGTTATATA AGAGGAGCTA AGTCAAATCC GGGGATAGG 579

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

CAGCTTATTT TGATGATTTT TGATGGAGAC TACATTTAAG TCTGTAAAAT GTAAAAACGC 60
TTGTGTTCTT TAAAGGACAT TTATTGTTCT CAAGATATGG TTAAAAACAC ACATTTAGGA 120
CTTGAGAATC CCACAGTAGT CTGACATTTT ATTTCCACTC TAACACAATC ACCCGCCATG 180
CAGGCTCAGA ACTTTCTTTT TTGTGTTGT GGCAGCCTTC TCTCTCTCTC ATATATATTT 240
CCTCTCTCTC TCTCTCTCTC TTThGnTCTC TCTCTCTCTC TCTCTTTTAG AGAAAGAGTT 300

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TATTGGGGAA ACCTGACAGG CTGGAGGGAA GGGGCAATGA ATGAAAAGAG GCAGTATGAA 360
AGCATTAGGG AGAGGCAGAG ACAGAGACAG AGGTCAGGGA GATGnGAGAT GTGGGATAGG 420
GATGGAGATG GTCCCGATGA GAGCAATGGA GACAGAAAGA GAGAGACATG TTCAGGAACA 480
GGTCCTTTTA AAACCTTGCC CAGGGGCAGG GGAGGGGAAG TAGGAACAGG GGAATCCCAT 540
TAGGAAGGGG GTGGAGCTTG AACTGGTGG TTGGGCCATG TGG 583

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

TcTAAGAAG GAAACTTTAA GCCTTGATA AATGAAAAAC AACCTCTTGT TCTCAGAGAT 60
AAATCATTAC AGTGAGAACT TTCTCTCAA CTTTTAAAAA AAGCAGAATG CTAATCTTTG 120
GCTTTGCATG CTAGGGTTTC CCTACACTGC ACGCACTCCA GTTCTCTGCC ATTTTGGTGG 180
AGGAACAGCT CCTGTGGGTA AGTGATTTAC CTTCCAGCCC TTCCCCTGCG GGACCCCAAG 240
ATCTTTAACC ATTTAAGCAA TGGCATTAA GTCTTAAGAA CCCCAGAAG CATGCCCCCT 300
GGCTTTAGAC ATTCTCAAGT TAAAAAAG AAAAAAAG GCCAGCTTGG GTATCAACAA 360
AGCAGAGAAA GAGTAAGCCA GATAGTTCAG TTCTGATAAG GTTGGAGATC TGCAGCTCAG 420
GTAAGCTGAA CTGTAAACAA GACCCCTTCT TGCTTCTGCA GGGCCCTGGC TGCTGCACCC 480
ACG 483

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

ATCCTACTAA ATTACCTTTG ATATACTTTT CAATTGACCT CTCTGCTTTT TGTTTTTCTT 60
ACCTTTGTGT AAATCCTCTT AGTTCATCCA AACCTTTTTT TGATTGCTCA GGTTCTCTTA 120
CTCCAATAAC TAGGGAAATC ATGTGGCTGG TAGTTCTTTC AACACACCAC ACAAAGAAT 180

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GCTCAGTAAA TGCTTACTAA ATAATGAATG AAATGCCTTA CAAAGCTAGG GTGAACATTT	240
AACCCGCTTG GCCATGAATG ATTTCTGTTT ATACATTTCA ACCCTGTGTC ATTATTAATA	300
TGTCTCTTTT ATGATCAAAT TTATCTCTGA GCAACAAATT ATACAGTCAT CTAATTGTGG	360
CAGTTATCAA ATATATATCT ATTTCAATTG CTCTTCAACT AGGTAGTTCT GGGATCAGAA	420
ATGTATTTGT TTAATTTTAT AGCCTCATTA TTCATCAACT AAAAGAATGA CTATCAGGAT	480
GCTGAGTTTT AAGTCAAGCA AACAGTTTCT GCC	513

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

TAAAGAAATC TTA AAAAATA TGCCAAAAGT TCACATAATC AGCTCTGGGC AAGACAGGAA	60
GGTAGATAAA AAAATATGAG ATTATCATTC ATTTTAGAAA GGGATTGATG GTGTCAAAG	120
TTAACTGTGG GGCCTGCACT GTGAGACAGC AAAGTTAAAG CCACAGCCTA CAGTGCTGGC	180
ATCCCACGTG CACACTGATT CAAAGACTGG CTGCTCCACT TCTGATCCAG CTCCCTGCTA	240
AAGCACCCAG AAAAGCAGTG GAATATGGCC CAAGTCCTTG GCTCCCTGCA CCCATGTGAG	300
ATACCTGAAT GAAGCTCCTG CATCATGGCT CCATGCTTCC AGCATGTAAA AAGAACTAG	360
CTGAAGGCAG AACATGAGTC AAGATGTTAC AGGATTGGGG ATAATCTGAA AAGAGAAAGG	420
TAGTGTGATT CTGTATCCTT GCTTCCTCCT GCAGCTCTGA ATCTGTCATC AGGGATTAAT	480
CACACCTTAA CCATGTACAG CCATTCAGAG CCATGACATA TATTCTGGGA ACGTGCAGGG	540
GTCTGATCCA CCTGACTCAA GCAGCCCTT CTTACTAATA GGAGTTCTAC CAGTCTAATT	600
TTGGGCAGGG AAGGnA	616

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

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TTTCTGTGTG TAnTTTTTCA AATGAATAAA TAAATCTTTA AAAAAAAAAAG GCAGCAGTCT	60
GCCATAATGG TGGATTATAC TTTGTAATCT ATCTGGAATT TGCTTTGATA AAAGATATGA	120
AGTAGTGCTT TAACATTTTT TTAACTTTTT TAAAGATTTT TTTTATTG AAAGACAAAG	180
TACAGAGAGA CAGAGAGACA AAGACCATCC ATCCACTAGT CTACTCCTCA AATGGCTGCA	240
ACAGTCAGGG CTGGCCCAGG CCAAACCAG GTACTTGGA CTCCGGGCAC AGTCTCCCAC	300
GTGGGTGCAG GGCCACAAGC ACTTGGGACC ATCTGCCGCT GCTTCTCAG GTTCATTAGG	360
GAGCTGGATT GGAAGTGGAA CAGTGAGGAC TCAACCTGGG CA	402

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

GTGGCAATGA TTAGAGTAGG TGGTCCTTG CCACTGATGT GGGAGACCAG ATAGAGTTCC	60
TGGATTCCTG GATTGGCCT GCACCAGCCC TGGCTGTTGT GTGCATCTGC AGAGTGAACC	120
AAAGGATGGG AGTCTCTCC CTATTTCTCT GTCTCTCTT CAAAAATAA AAATAAAAAA	180
ATAAGAACAG AAAACCAATT GTGTGGGATA AACCCGTATT CCTCTCCTT CTATAACAAA	240
CACCAGGAAG CAGGATCCAC TTCCAGTTC CTAAAAATG TGAATTCAGC CAGTAATGGG	300
GCTATTGAAA CTTCTGAGAA TAATTAGATT GAACTTTTCA TAAAGATAAT CAGAAAGTGG	360
AGGGAGAAGG GAGCAACATA ATTGAAAGTA GTGACGAAAA ACACACAAGT GTCTTATAAA	420
ACAATAAAAT GTTTATGTTT TATTTTATA CCATCTTTCC AGCAG	465

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GCTGTCTTCT GTTACTTTCT CAGGCACATT TGCAAGGAGC TGGATTGGAA GCTGGGCAGC	60
CAGGACTTGA ACTGACCTTC TGACATGGGA TGATGGAGTC ACAAGTGTTT ACTGAACGTG	120

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TTGTGCCACA ACACAGCACC CTTTGTAGAT AAGTGTATAA TTTGCTTAGG TTTTACAAGT	180
ACTGGGTAA GTCCATTGCC CGAGTAATAT GGCTAATAAT GGCAGAACCT CTCTGTCTAT	240
GGCCAAATGC CATGCATCAG TCACTTCCAC GTAGGCATAT GTTATCAGGA GTGGTCAAAC	300
GGCTACGTCG GTGAGCTTTT TTCTTCCAAA ATAGGAAACT TTTGTGCTAA TCAGCAGAAA	360
GCACTGATTT AAGGAAGCAG TGATCTCTAT CAGCTCCAAA AGCATCTTCC ATAGATGTCC	420
ATTAGTTTCA C	431

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

TGACCTTGCA CTCACTTGGG AGACCCGGAT GGAGTTCAG GTCCTGACT TGAGGCCCGC	60
CAGGCCTAGC TTCAGTGGTT GCGAGAATTT GGGGAGTGCA CGAGTGTTGA AGATCTTTCT	120
GTCTCTCTCT CTCTCTGCCA CTCTCTTTCA AATAAATAAA TAAATAAATC TTAAAAAAGG	180
AAAGAAAAAT GACTCCAAC GCTGTGGTGG nGAGGGGGG AAGGTCCCA GCTGTATTTA	240
CTCCAGGTTT TTATCTCCAT GTGAGATAAA ATTCAAAGTG GAGTCATATA TTGAATGCAA	300
AAATGAAAGG AGGATTTATT TAGAGAGAGA ACATTTGAAA GTTAAACATG GGTAGCTCTG	360
TGAGGAGAGG CACACACTAT AAGGAGCAGC ATTTGTAGCC CAGTTCAGTG GTCTCTTTTA	420
TTGGATAGGG GT	432

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

CAACAGAGT AAATTTACTT CTTTGATTCA CTATGATATT TTTGGAAGAC AATGAATTAA	60
AGACAACAGA ATGGGAAATG TTTACAATCT TCCAAAACAC GGCGCCATTT AATATCTATC	120
TAATTTTCT AGAGTGAAAA GGAATCATAT AAATATTAAA TGGAACCACA CGAAAGTGCC	180

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AATATTTGAC TTTTTTTACT GTTAAGGGAC AGGGTTTCAT ATGGCTCACT TTAATACATT	240
CAGAGAAAAT GTTAACAAGA AAACCTCTG AAGGCACGCA TCAGAAAACG CTGATCGGAC	300
GAAAGCAATT CTAGACTTGG CACCCTTAAT GACTGCACAG TAATGGCCTG GTATTATAAA	360
GCCCCAAGCC CCACTCTGTC ATAAAACATG ATTTCCCTTT TAATGTTTCAT TACTTAGAGA	420
CACTGACAAA AAAATCTGAA GATAAATTTA AGCTCATAAA TACCATGnAC ACAACATACT	480
GTAGCAGAAA TAGATAATTT GCTTCACTAA ATTAAGTAAA TAACACAGAG TAGGCTATAC	540
CAAAGAATTT TGGCAAATTA TGGATA	566

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

TTCCATGGTA CAATTCATA TCATCTGCAA ATATGGATAT TTTGACTTCC TCTTTTCCAT	60
TTTTGATGCC CCTTATTTAT TGTTCTCCC TAATTTCACT TGTGATTCT TTCACTTGTT	120
GATTAAAAGT GGGGAAAGTG AACATCCTTG CCTTATTTCCA GATCAGAAGG GAAATGCTTT	180
CAGCTTTCCC CATTCCATAT AATATTGGTC ATTGGTTTGT CATAATTAGC CTTTATAATT	240
CTGAGGTATT TTCTTTCAGT GCCTAGTTTG TGGAAGTTTA TATTTTATCC ATGAAAATGT	300
nTAATCTTGT CCAATGGCTT TCTCACACTT ATTGAGATGA CCATACTCTT TTATTTCTTT	360
ATTAAATTGA GAAGTATGGA TTAGCTCTTC CAGAAATGTT TTCTAGAATC ATnTGTAATG	420
TCATTAGGTC CTGGACTTTT CCTTAATGGA AGACTTAATT ACTGCGTTAA TTTCATTGGC	480
CTGTnATGGG TTGGTTTGAG GGTGT	505

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

AGAAGGGACT GCACTGGGAT GGACCAAATC AGCACAGACA ACATCTTCAA CAGTGCTTTG	60
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CnTnTAGTAG GGGTGAAAAT TGCCATTGAC TGATTAATGC TGTCTTGAGA ATACCGGATC 120
 ACAGAATGCA AAGTCACTTG GGTCTCTCTG ATTCTATGT GGATTGCAA TCATCTCTGA 180
 GCTGCAGGAA AACTGAATTT CATTAAACAG TTCCCTACGC TGCAGCTTTC ACAGTAATTT 240
 GAATGTTTCC AGTTATTTTT CAATAGAAAT TATTCTTTTC TCCGGGGACA AACAGGCTT 300
 CATCCTGTCT ATTTCTTGGC TGGTCTAAGA ATCTAGGTCA TATATCATTT GGAGATTTCA 360
 CTCGGGCTAG AAGGGAAGGG ATAGTGGTTA GCTATTGCAA CAATCTCTAC CTGGACCATG 420
 GAGGAACACT GGATTAAGCA CAATTCTTGT CTTTGGGAAG TATGGCATAA CCACTACTTA 480
 AAGGGCAACA GACTCTCAG AGTTCCTGGC ATTTTTCCTC CATGTAAG 528

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

ATTCTGAATC CCATTTGCTA GGCCTGTAAT GTCAATTTCA CAATGAGTCA GCCCTCCATG 60
 TCCACCTCCT GCTAAATCAG ACCTCCTCAT CTATTAATCC GTGGTAGAAA GCTCTCCCAG 120
 CGTACTCCAG AGCTGGCTAT GAACTGATAC CCGCACCGTT TGGCTTCCAG AATTGCAGGA 180
 CTCCAGAGTG CAAGACTTAG GCAGACACAG TCATTGTCTAG AGCCTTGAAA GGAAGTGACA 240
 GCCAGACGGA GGAGGAGTCA CAGCAGAAAGT GGTCATCATT GCTAGTACCA AGGCTCCTGT 300
 CTGAACCCCTG CCTGCCATGT CACTAGCAAA AGATGTGAGG ATCAGTCTCC TATTTT TAGA 360
 ATCTCAGCAT CGCATCGTGT TGAGGAATTC GCAGGCTAAA CTACTAGCCA AGCTGGGATT 420
 CCTCCTGGAT GTCCCTGGAT CATGCTATCA GACTTGTCTT TTCTCCTTCC CTCTCCCTCC 480
 AGCCTACATT TCAGCACACT CCTGTTCTAC CCTGGCTGTT CCATACTCCT CTAATCTAGT 540
 CTGCTCTTTT TCTCTGTCCA T 561

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

ACGTCGTGGA GCACnTGGTT GTCAAGGTTT CCTCACTTGG GGTTTTCTTC GTCATTTCAT	60
CAACGTGTGC TGGTCCTAGG AGAGACAATT GGAAGTGTGT GCTCTCCAAT CGGTGGGTGA	120
GAGCAGTGTC ATCTTCGCAG GCTGATGAAC CACCTGGACC AGGCAAAGCC TGAACGGAAG	180
AAAATGGGGG CGATGCCAGC CAAGCCCATT TCTAAGTCAG CCTCTTCTGA ACCAAGCACT	240
CTGGCTCCTT CCTTCCTCTT TTCTCCTCC CTCTTGCATC CTCTTTCCCC ATCCCTTCTT	300
ATTTTTTGCC TCCTCTCTGT CCTCCGGTTC TTTATTTCCT TCTCTCTTTG TTTGTCTCCC	360
TTATTCTTGG ATTCTTTGTT CCTTTTGTGG CAAGGCAGAA CTAAAATAAG GTAGTTCTCA	420
AAATTTCTGT TTTTGGGGAT TTGTCCCAAG GCGTAATAAA AATAAGCACA TTAAC TTGTG	480
ATATCAGATC GGAAGTCTAA TACATGAGCT GGGTTTGAAG TTG	524

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

TAGCATTCTA CCCAGACACC CTTGCTTTTC TGCCAGACAT AATCTACATG AATCAATCCC	60
AGGTCTTCCA ATACAATGTA GCTTGCTACT TCAGGAGCTG GATGGTGTAC AATTGTTTAC	120
AGATGCTCCT AATTGCACCT GGATCCAATA ATAAC TAAAT ATTGTTTAAA GTTTTGGCAG	180
CAACTATTTC AGGAGATATG TAGGATGAAT GGTGAAAGT AACACTCCAG GCATAAACCT	240
GCATGAATTA GAACCTGTAG GAAACATAAA CACAATTCAG TAGGTGGCAC TATTCCCCCA	300
GTCAGAACCT TCTTCATTCT GCATGACTTG GCAATGACCT TTATTAATTT ATTCCATGGA	360
ATTCTGTGAC CTCAATGAT ACCAATATAC TCCAAATACA TATTCTGGAT TCTTTGAGAT	420
ACCACAGCCC AGGTAAGAAA CAATCTATAG TAGCAGGTAT AAAAATACAA AATCATTGGT	480
TTCATCTGAA GTCTAAGGT AATCAGATCA GCAGGTACT TGAAGTTAAT TAATTTCCAT	540
CCCCATCAAA CAACCCAATT GGA	563

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

ATTCAGCTC TCATATCTTA CTTCTCAAAC TTTAGCTAGA TTCCAAAAGA ACTACTCTTA	60
TTGGCAACAA AAAGAACTAT AATTCCATTC ACAGAACTC CATGTTAGAA ATGTATTCAA	120
TCCAATCCCC ATTACTAAAA TAACATGTTT CATTATTTT GTTCATTTA CTTTAATAAT	180
TGTGTAAGAA TTAAAAATCC TATGTCCTC AGAAACTCA TATTTCACCC TTAAATGGC	240
CATTTCTAAA TGGACTAATT AAAAAATTA AAAAATTAAC TCCTCAACTT TAGAACATTG	300
GAAAATGAAG AATATGTCTT CTGGGAATTT AGAAATGTT ATTGCAATCT TATTAATCCC	360
CTTATTTT GAGTGTATAA TGTGCTCACA GTCATCTAAT CCACACTAAT CAATCAAAAA	420
GCTTTTATTA CTGAATGTTG CAGTGTTCAG CAATGTCCTA GACACTGGCA GGCTTAAAAA	480
TTCTAGATTA AGGCCGGCGC CGCGGCTCAC TAGGCTA	517

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

CATTGCTAAA CCTTAATCAT GGTATCATTC AAATAGTAAT TTCTTAGTCT TTCACTTGGC	60
CCTTCCTTTT GTTTTACATT AACGGTTTTT GTCTCTCTCT CTCTCTTTT TTTTTTTTA	120
ATAATCCATG CGCCCCAATT AAGTCCAACA TCGCTGATTT GGGGCAATAC AGAATCCACT	180
GCACCATCTA ATCTGAGTAT AATTAATCAC TGCATTTTCG ATACCAATGC CCAATCTGTA	240
CCCACAATCT TCCTCCCCTA AACTGTCGCT CCTGCTGGAT GCTCTCTAGA CACACCACTG	300
GCCCTCACTT GATATTCAC ATCCCCTCCT GTCTGGCAAC CCCGAAATCA AACTTTCTCA	360
TCTCCATTGG AAAAGTAATT GCTCTTAGTA ATTAATCTTG TTATTTTCTT GCTTAAATAC	420
TTGAGTGAAT TCCAAGAATG TATAAGTAAA ATTCAATTC CATAATACTG TACTnTA	477

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

TGTAAAGTTT AGGACAGTAA GTGTAAAGTC ATCCCTGGAG GATAAAGTTG AGTTTCTGTA	60
TTTTGCTCAG GAGACAGCGC TGTTACCCCG GAAGGTCACA GCCTCTGTAT TCCTGTGTGG	120
TAGAGGTTCT GCTGTTTGTG GACACTTGAG CTACTTTTCC CAGCAAACGG AGCAGGACAT	180
AAAACCTTTC CCCTTTCTGG GTTGTGTAGG CAGAAACAGA TGGCTAAAGA ACATCTTAAG	240
ATTAGACACA GGAAAATGCA GGTCCCCTTG AATAGAAAGG AGTCAGTCCA TGCTGCTAAA	300
TGAGGCATCC AGGCATTTTG TAGAGCATAA CAGAGAGGAA GAAACCTAGG TTAATAGTTA	360
CTTTGATTTA AATGAAACTG TCCCTAAGGC GGCTTTGAAA TGAGACGGAA GAAGGACTAT	420
GACACCAGAA TGTATGTTCC CAGCACAGAA TAGTGTGAGC TGAGGGACAT GGCAGCAAGT	480
CCCAGGCTC AGAACACAGA GATTCTCCTT GCTGTAGTCT AGAGCAGGGA TCTCATCAGC	540
TTCTCATCAG GTACAAATG GAAAGAAACA CAACTTACTT TATATATATn AGCCnCATAT	600
ATATGTGTAT ACACACACAC ACACACTG AGGGCTGAAA TTAATGC	647

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AAAAAGAAGA GTATTCAATG GGAAGGGCC CCCAGGTAAT CACAGCAGTA ACCAGCTCAA	60
TCATACTCCC TTGGGTTGCA CTTTCTTCTT TCCATTCTAC ACTTTTCATT GTCTCACTAT	120
TGTCCCCCTG CCTTCCCTTG CCAAAATAAA CTCAAAACTC AGAAAATATT AAGAGCTTAT	180
CTTAGAGTGT ATGCAACTTT GAGTTGTCCA TTAGATGTCC AAGTGGAGAT GGCAAGGAGG	240
CAAGATGACC TAGAGTCTGG AATTGAACAC ATAATGTGCA GAAGAGACCA GGTGCTTGT	300
CTTCAAAGAT CACTGTTTAA GGATGTGTCA GAACTCCCA CCTTCAGAGC CTCCCCGAT	360
ACAATGCATC TCCATCTCCT GTTGCTTTGG TGAACACTCC TTTCTGGTTC TCAAGAGGAG	420
CCAAAGAAGA GGCCATGCTC ATGGAAGGCA CAAAACCTG TCCTGCCATT CTGATGATT	479

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```
GGTCTAGTTC CAATATGGGC ATTTGAGGAA CTGCATCAGA TCAGAGGAGG ACATTTTACA      60
GGGCAGGAGG GCCTTTTGCA GCAATGTGGA CACTACAGAT ACTATCTGGT AGAATGCTCA      120
GGAGAATGGG CTCTGTGTGC CATATACCAT TTGAAACCCC TGCTGAAACC TTTCAGTTGT      180
GGAACATTTT TTTTCATTTA GGTAGAATAT GTAGAATTTT AAGTGTCAAA AATCCACTGA      240
TGAAGAAAAT GTTATTCAAC TTTTCCCCTT CCTGTTTCTT GTTTTCCCCT TCATGCTTCT      300
CATGAACAGT GGTCTCAGCA TTTCTGTATG GAAACCTAG AGAGTTTTC AGTGTTTTTC      360
CTTCTAACGG TCTCAAGTGA AATTCAGGG ATATATTATC AAAGTGCAAG TTGGTTGGCA      420
TGTAAGTTTC TCATCCCTAG GGCAAGATGG CTTATCTCTC AAGCCAACTC      540
CCAGTGGATT TTTGGTTATT TTTTGTGnTT CTGTTGTGAA CTGTGAAGTC ATTGCTACCT      600
CTGTAGGAAA GAGGACCGTG AGTGGCTAnG TAGGGTCAGC TGGAGA      646
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(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

```
ATAGAATTGA GTACAACTTA AGCATGTGAA CTCTGAAAAA AGACTTGCCT AGGTCCAAAT      60
TGTAACCTCT CCATTTACTG GGCATGGGAT CTTTGGCAAG CTACCTGAGT GTAATGGGCC      120
TTCATCTGCC CCTCTGTCAA TAGGAGAAAA TAATGGTGCC AATTTAATGA ACAGCTATGG      180
TTGTTAAATG AAATGATGCA CATACAACAG CTCACAATAT GAACCTCGTG AGTGATTATT      240
CATTATTATT ATTTCCAAAG AAAACTTAAC AAGTTAATGG GACCAAATAC TTCTGTCTGG      300
GGTGCAGGTG GGGGCAAAT ATCTAAATTC TGATTTTAGG AGAATTTGAT CCAAAGTTTT      360
ATAGTTTCCT GTTTTAAAGT CCTTGGTGCC ACTGTCTCCT CTGGTACAAA TTCAAGTGAT      420
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CATGTCACCT CCCAAGAAAC TTCCTGCTGG AAAAAAATG TTTTCTAGGG GAAGAA

476

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

TGCCCCnATC	ACGCATCCGC	TCAAAGAAAA	GCACATACCG	AATACACCGC	TCCCCCGCCA	60
ATTGCTGCAC	CGCAAGTGCC	ACACCAATTA	TTAGCAAGAG	AGTCCAACAC	ACCGCCCTCA	120
CTACACCGTA	CAATGCTGCC	CCATCCCCCTA	TCATAAGGGT	CCGGTAAATC	CCCCCGAACC	180
TTCAAAATAC	GTGATAAAAG	AAACAAGCCC	ATTGTAGATT	CCCTGCGCGC	ACCTTTTCAA	240
GTAGTCCGCA	TCGTTGAGCA	ACCGCGCCTC	TACCGGATTA	CTCACAAAGC	CTAATTCCAC	300
CAAAACACTT	GGCATCTTCG	CGTTCCGTAC	TACAAACCAG	GCCTCCTCTT	TTACTCCACG	360
ATTTTACTT	TGTGCACCGA	CGCTTGCTTG	CATTCCGTCA	GCGATACTGC	GCGCAATCAT	420
AATACTTTCC	ATTGTGAATT	CCTCTTCGAG	CATCGAGTTC	AAGATCGGGA	GCACCT	476

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CTTACTCACC	ATCCCTTGAA	GGGCAGGCGA	GGGATTGGAA	AGGGGGGAGA	AACAGGCAGG	60
GAGCAAAGGA	GGCAGTGCAT	ACTGTTGAAG	ACTGGAAGGT	GTACACAGAC	ATAGAGGCTG	120
CATGGAAAGT	CCATAGGAAT	AAAGGAAAAC	CCCAATCATT	GGCTTACAGA	AACGGGCAAA	180
AGGGACAATG	TGCAAAGACA	GACAAGTCCC	TGTCACTTTT	CTTCTGAGAC	TCAGGAGAAT	240
GCCTGAAGCC	CAACACATGT	ATACATTGTT	TCATATTTCA	GTGAGAGAGA	ATATTAATAG	300
TACCCATTTA	CCAAGTACCT	TCTGGATGCC	ATCTGATCCT	TATGGTCAGT	GTTACCATCT	360
CATCTTACTC	AGAGGACTCT	GAGGCTCAGA	AAGTTAAATA	ACTGTCTAGA	GTCACACAGC	420
TGTAnGGACA	AAGCCCCTAT	CTATACTCAG	TCCATCTTCC	AGTTTATTTT	TCTGGCTGTC	480

CACTAGCATC TATTTCTAAA ACAGCAA

507

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

AACCACTACT GTATATTTTA AAATCAAACC AAAGTATAC ATAGTTATCT GTTGCTATCC	60
AAACCTATTT GGCACCCAAG TTTGCACAGC AAAGGCTGGT AAGGGGTATG CATTCTCTAA	120
GGCTTTTGA TTCTGAATT TTGAACAGCA AGTGGTGAGA GTTTTGAAA GCAAGAAATT	180
CACAATTCCT TTGTTACCTA ATTTTGCCT GGAAGCGTC TGGTAGTGAG GTAGCTCAA	240
TTGCAGTTT GAGGCTGCAC TTGGATGCCT CATTTATGAC AATTACTTAA AGTGATTAGA	300
CTGGGTGCCA GGAAAGGAAC TGAGCATTTA TGTGTGCTCT TTCCTTTGGT CCCCATAGGA	360
ATCTAGTTAG GCACCTGTCT TTGTTATCTA GATGAGGAAA GTAAAGGAGA GGTATGCTGA	420
CTTGCCCTCAG TCACAAAGTT AGTGCCAGAT GGAGCCAATT CACCGACACA AATATGTGAC	480
TCCAAAGCCC ATGGATCGGT TTTGTCAATC TC	512

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

AAGATTGTCT AACTGTGCGC ACGTCTGAGG CATTGTGAGG GTAATGCCCA CGGGTCTGTC	60
CCACCTGAGG ATCCTCCCTC ACCGCCCTC CCACCTACGC CTCCCCCA CCGCCGGGGC	120
TGATGGCAGC TTCCTTCCTT CCAAGCAGTA ACGACTCTGC CCTTTTGTGT TAGCCACATC	180
TTTAATTTTC TTTCTATTTT TGGCACCAA GTATCTCTCC AAATAATATA ATTTAATTTT	240
GTTTCTGAAC GTGAAATACG TGAGATCATC CAGGATTCGC TTGTGGAGTT TGCCACGAAA	300
GGAATAAGCT CAGCTATAGG CAGTGTTCCT CACTCCTGAC TCTGCAGCGG CCGTTGGTGG	360
AGGCTGGTGC GTGTGCCCGG GCGGCCAGAG CCTCTCCACA GGGCACCACC TTTCCCCGCG	420

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TGGCCGTTTC AGCTCTGCCC TGCAGTCCGT CTGTGGTCCG CATTGTCCGA GGTGACCGGT 480
CATCGTGGTT TACGTCGCA 499

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CTGCATAAAA CTGCTGCTCT GAAGTATCTT GCAAGACAAA TGCTTTTACA AAATTTGCAC 60
CTACACATAA TTAATTTGGA TAAATTATGA AAAAATGGTT TCATGGAGGG GAAATAAGTC 120
ATTTCTACTT TGATTTTGTG TATCTTCTAT GAACCCCATTA ATTGTCTCAA TTTACTGTAC 180
TAATTTTCTC TTTGCCCAGT CTTCAAGTTT TCTTTTGCTT TCATTTCCAGA CTTAAGGTTT 240
ATGACATTTT CAGCACCACC AAGGTTTGAC CAGAGTTCTT GTAATAAGAA AAATCAACAG 300
CTGTGATGTA CATAGTATTA TGATTACATC TATGTCCAAA TTTTATTTTA AGAATTGTGT 360
TTGTTATTAA CAAAATAAAC TCGCAGGAAT GATGTCTGCT TATATGATTG ATTAGTTTCA 420
GTCCTAAAAT TATAAAGAAT GTGTTTAAAA ATAAAGATGT TTTATGAAGC TCTTTCTTCA 480
TTTGAAGAAG CAGGATTTT CCTCCAGGTC TCAGTATTTC ATTGTGG 527

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

ATTATTATAA TTAGTATCCC ACTTAATAGG TTCCAAAATT CCTACTTTTT AATTAAATAT 60
ATAAAGTGAT CTGCATAATA TAGAAGTTTC AAATCCATTT CTCTAAATTA AAAGTCCAAG 120
TTGAAAAATC GGGTTTGGTT AAAAGCTGTG GAAGGAGAGA AATAAAATAA AAACCGTTAA 180
GAGTTAGCTT TTATTGAGTG ATGGATTAG AATGATTTTC TTCCTCTGTG CTTTCTGCT 240
TGTCAAATTT CTCTAAAATG AGTACTAAAA ATGTAAACAC AAACAATTTA AAAAGCTGTA 300
TGTCAGAAAT GTGAATGCTT AAGTAAGCTT TTAATGTTAA AAAATAAATA AATAAAGTCT 360

919

GAATTATACT ACTCCAGATG GCTTCAGCTG TGATTTCGTGC ATAGCATTTG AAAGATCGTT 420
TTTTTACATA AAATACCCAT AACGCTAATG TACTAACACG GAGGTCCACC GGACTCCCGC 480
TGGGTTTCTG AAGGGAATGA AATCTAAGCC GTTAA 515

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

GGTTTGCTGA GGTTATTGAG TGTGGGATGG GTGTAGGTGG GGTTTGAGG GATGGTTAGA 60
GGTATAGGAA GAGTTTAGAG GGGGGnTGAG TGTATATGAT GAAGGGGGGG GTTTTATGAT 120
GTTGAGTGTG GATATATATT AGGTAGGGTT AnTTAGGGG 159

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

AGCACTTGCG CGCAACCCCTG CAGCTTGCGC nTCAGTCCCG CGGCTCGGCT TCCGCGGCTC 60
GGCTTCCGCG GCTCGGTCCC GCGGCTCGGT CCTGCGGCTA GGCTTTCGCG CGCGGTGGGC 120
GACCTTGTTT TCCAGTAGG TCCTCCGATT TACGCCCACT GGATCCAGAA GAGTTTCGTC 180
TGCAATATTT TCCTGGTTCT TTTTCTGAG GCTACCGTAA CTCCCCTTTT ATTAACTAA 240
ATTTTCCCGG ACTATCGGTG CGCGCCCTCA CTATTCGCC ATCTTGGCTC CGCCCCCAG 300
TAGTTTTTTT TAAGGTTTTT ATTTTTTATT GATTTGAAAG ACAGAGTTAC AGAGAGAGGT 360
AGAGA 365

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

AAAGAAGAAA ACAC TGCAAA TAATGTTGAT GAGCTCCAGC TACTGGTAAA GATCTTAGGC	60
TTGACCAAAT GTGATTGCT GTGTTTCTG TTTTGCTTCA TTCATGCTGC TGTAACAAAG	120
GAATAAGATT GGGGGGTTA TAAACAACAG AAGTTTCACT GTTTTGAAG TCTCAGGTCA	180
GTTTGCCAGC AGGGCCGGT TCTGGTGAGA GCTGTCTTCT TGACTGCTAA CTTCTTAATG	240
TGCCCTCACA TGGTAGAAAG AGCACTGAAG AGCTCCCTGG AGATTGTGTT TTAAGGGCAC	300
TAATCCCGTT CTTGAGGACT GTACCCTCAT TAGCCAGTAA CCTTCAAAG GTACCACACC	360
AAAATATGTA TGA	373

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

GCTAAATCT CACATTTTTT TTTCTTTTGT TTAAAGGGAA ATCCTCACAT TCACCTGATA	60
CTCAGATGAA TGTGAAAGTT AAAAATCTTC TCATTCAAAA GAGCACACAG CACAGATTGA	120
GTAAGAATGA AAATGCCTGT GGAGACACTT CTGGGTGGTC CACATTGTAT ATTGCCTGTA	180
AGTTTCACTC TTTTCTTGTC AAAGACTTGA GATTCCATTC TAAAAATAAA TCAACTCAGT	240
TGGGTAAAC AGTCCAAAGA AAACAAAAA TTTATTATCA AAATAATAAT CTAGGCCTTG	300
AATATTTCTT TCTCAGACTG AACTGAGATA TTTCTAGAAT CAAAGCAGAT GTCACCCATC	360
CTGACTAAAC TACACTATTT GCTCTGGACT TATATGAGAT TTTTCCATTG GTGGCTGCAA	420
TTTCCAATCT CAGTGTAATA TTACTTCGGA TAAAGACAAC AATT	464

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

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TCATTTTTAT TAATCAGCTC CGCATGAAAA TAGGGATTAT GTTTGGGAAT CCTGAGACTA 60
CTACnGnGG CATTGCACTT AAGTTTTATT CCTCCGTGAG ATAGAGGTTA GGAAGGTGGA 120
AACGCTTTCA AGAGGTGATG AGGAAGCGTG GGGCAATAAG GTAAGGATCC GGATAGTAAA 180
GAATAAGATG GCACCCCCCT TCCGCAAGTA GAAACGGAGA TTCTCTTTGG GAAGGGTTTT 240
TCTGCCTTTT CGTGTTTGCT GGATGCAGCG GTTAAGCAGG AAATTATCGA AAAAAAAGGG 300
GCGTGGTACG CGTACCGAGA AGAAAAGATC GGACAGGGGC GTGACAATGC CGTGGGCTTT 360
CTGCAGCAGA ATATGGACAT CACCTTGAG ATCGAACGGG CAGTGCGTAC GAAGCTTTTT 420
CCTAAGCAGG CGTTTATATC CAGCTTTCAG GAACATCGTC CTGCTC 466

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

CGGATACTGG GGAGCGGTGT GCGGAAATTT TTGTGTGGAC CGCGCGTATG TCCGCTGTAC 60
CGGGCCGTGT GGTACCGTT TGTGTACGTG GGTGCCGTGG GGAGTTGAG TAGCGTGTGG 120
AATATCTCGG ATGCGTTCAA TGGACTGATG GCGTTGCCGA ACCTGGTGGG GCTGTTATTT 180
TTGGCTCGTC A 191

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

CATGTAACTC TGCCTTTCAA ATAAATAAAT AAATATTTAA AAAAAAGAAA ATGTACATTA 60
ATATAAAACA ACTTACAATC TACACCTAAT TTGTTGATGG TAAATAGGCA ATCTTCAAAT 120
TTTCAAATTT TCCAGTTGTG AATTGTCTG CTTGCTGAAC TCTATTTGCA ACTCCAACT 180
CAGTGCTCAC AACACTCACA GGCACACGGA GAGTAGGAAA AAAAAAGGC AAAATTCAGT 240
CGCAGAGGAG GCTGCACGAG GCCACACTCG GTCTCCTGAC GTTACAGCCG CGTCCTTCGG 300

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GGGTCTCTGT GTGCTGTCGC TGGTGATCCA ATTGTTGCAA CCAGTGTTC TGCTCTGTTG	360
CACACAGGGC TGTGGTCTCA CAGTCGGGTG TGGTCACAAG GTCTCCTTGG ACAGACACAC	420
GTCCAGCCAG GGCGCACAGC GGCGCAGACC TGACAAAGCC GTGTGTGCAG TGA CTTGATA	480
AGCGTAATC CCGCCACCG CAAGAACTGA GAATTGAAGG GAGACAGACT GGAGAGACCA	540
ACAGGGAGCT GACCGAACGA GTGATATCCT CCATGCCAGA GCAAACGGAA GAGGACAAAG	600
CACAGGCCAG ACCGCCTTGT CCTAA ⁿ TGGA G	631

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

CGCAGCGCGG G ⁿ CGAAGGCA CAGTGAGAGG TTTCAGACAC GGATGCGCCG TGTGACGTCC	60
GCTGGGGAGC TGAAACATCG CGAATCCGTT CCTCCAGCGT TTTTAGGGGA ACACGACAGG	120
GGCTGGTGCC TGCCCC ⁿ TACG TCCCCAAGCT GTGCCGCTGA GGTCAGGACT TCTTTCTCCG	180
GCTCTCGCGC ACCGGAGCAG CTGGGGACCG CCTGTCCCAG GCCTCCCTCC CCGCTGCTCT	240
CCCCAGCCCC GTCCGAGGAC TGACCTCCCA CCGGTGAGTG AGGGCGGTCA GGCGGGGCTC	300
GTCTCTCTGG GTCTCGCTCC TAACACAGCG ACAACCTCTT AGGGGAAGAA ACGCCTCTTG	360
TCAGGGTTCA GTGAGACTGG GGACCCCCAA TCCCCCAGAC CCCC ⁿ GTGCT TGCAGCCCAG	420
CCGTGGGCCC TGCAGATCCG CGGGAC ⁿ GC ACGTCCACAG TGCTTCTTTT CCGGAAATGC	480
TCCCTTCTGA GCCAGTGCTT CTGGTACAGT CAGAAT	516

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

ACTGTGCCAG AGCGCCGGCC CCCGAGTGGG TTCTGATTAA GATGTTTGAG GACCACAGTT	60
GGCCTTCCCT CTTGATGAGA GCCCAGAAAT TTCCAGTGA GAGGGGTGTG GACTTAGGAG	120

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ACACCCTGAA GTCCGGTGGC CTTGGTGACT TTGTCAGCGT CCGTGGTACT CAGCCGCTGA	180
GTCAGGACAC CCGGGATTGC TCCTACAGAG CTTGGATTTT CTTCCGGGCT GAGCACGTCG	240
GGACCATCAA AGCCAGCATC TCAGCCGTGG GTTGGTGGGC AGCGGCTCTG AGCAGATGAG	300
GCTCAGGTGG ATGGGTTTCCT CTTTCTGCCA GGGAAAATGC CTCAGGACCA CTTCTCTGCT	360
CTCCTGGGAC AGGAAGGCCA CAGGCTCATT GCGATTTTTA CGGACAGCAA GTCATCCTGT	420
CCGTGGGCTG GGAGGACTCC ATCTTCATAA TTCTGGAGTC CTGAGCTTGA CGTGACTGCA	480
GCCATTTTGG ATGCACTTGC TGTGTTGCCC TTGAGTAACT CTGAGGTCCT CCCA	534

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

TGTATGTGCA TACGTGCTTT CCCCTCTGT TGAATGCCTT CTCCTTCTGG TGAGCTTTAC	60
CTGCACAGCC TTCTCCTTCA GGGCCATCAG CTGCGCGTGG CTGAAACCTT GGACAGCCCC	120
CAGCAGCTCC ACGCTCCTGA TGAAAGTGTC TCCGTCCATG CAGAGCAAGT CCTCAGGGGC	180
CCAGCAGGCG TTGGCCTCGG CCAGCCTGAA GATGTCATTG GGAGAGGGAG CCACGACTCC	240
ATGGCAACCT GAAAAGTGAA TGGGGAGACG CAGGAGGGGA CGGGGGAAGC AGAACTCAGG	300
GCAGGTTAGC CCGATTCTCT CCTGGAATGA GGAATAACTC ACCCCAGTCA GATTTATTCA	360
CAAGATGCCT TTCTTGCTGG TGACCAGCTA CTAAAATGGT GATACCAGCT TCTTGACAT	420
CCACATTGCC ACTGGACCAC ACAAGCCAGT GCAGTGAGAG CTGGTGGTGG ATACTCCTGA	480
CATGAGATTC AAACCCAAAG CCACTnGnC	509

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

TTATGATAGG ATTGTCATAA AATCATTAAG TAAATTATTT ACCCATTTCA GCAGTGTGAT	60
-------------------------------------------------------------------	----

924

TTTTTTTTTC TGGCTCTTGT GCATTAGATA ATATGAATGG AAGGGAAGAC TGTTTTTCTT	120
ATTTAACCTTT TTTTTTATTT AGGGTAAACA AATTTCATGT AATTCACATG TACAGATATC	180
AGAATATAGT GCTATThCCC ACCCTACCCT CCCTTCAGCC CACAGTCCTA CTCCTTCTCC	240
TCCTTCCTCT CTTATTTTCA CTCTTAATTT TTATAATGAT CTACTTTTAG TTTACTTAAG	300
ATTAACCCCTA TATAAAATGA GTTCAACAAA TAGTAGGAAT TAAAAACAT GTTTCCTCAA	360
CAGTAGAGAC AAGGGCTGTA AACAATCATC AATGCTCAAA ATGTCAATTT CATTCCTATA	420
CATTTCATTT TTGATATTTT ATTAGTTACT GCCAATAAGG nAAAACATAT GGCATTTGGG	480
ACAAGCTATT CTACTAAGTA TAATGGTTTC CAGTTGTATC CATTTTGTTG	530

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

AAGCAAAAAC CGTGTTTCATG GATTGGAAGA AATTAATATC ATCAAAATGT CCATACTAAT	60
GAAAGCAATT TGCAGATTCA GTGTGATCCC AAACAAAATA CTGACATTCT TCTCAGATTT	120
AGAAAAATGA CAATAAAATT CATATGGGTA CACAAGGGAC ACAGAATAGC TAAAGCAATC	180
TTAAACACAA AGCTGGAGGC ATCACAACAC CATACTTCAA GACATACTAC ATACAGTTAT	240
AATGAAAACC TGAAATTGGC ACAAAAATAG AGACCTGTAG ACCAACTGAA CAGAATAGAA	300
ACTCCTGAAA TCAATACACA CATCTATGCC AACTAATTTT TACAAAGGAT CTAAAACCAA	360
TCCCTAGATA ATTGACAGTC TCTTCAACAA ATGGTGCTGG GAAAATCAGA TCTCCTGTGC	420
AGAATTATGA AAGAAGACCA CTAGCTTACA ACTTATACAA AAATCTAAAA TGGATCATGA	480
CCTAAACCTA TGACTGGTAC CATCAAATTA CTAGAGGGAG ACATGAACAT GGGGAAA	537

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

925

TGCACAGATC AAGAAACCAA ACTTTAAATT ACAGTAATTC ATCCCATATC ACACAGTAGC 60
AGAATTAAAA GTGGAGTGGG TTCCCAGCAG ATTGTAAATT CTTTGGGAA TGCCACCTTT 120
TTTTATTTTG CTTTAAAG TGAAGTGGTC AGGGATGGTG TTTAGCAAAG CAACTGTAAC 180
ACTGCTAAGA TGCCTACTAC CTCTATCAGA GTGCCAACAT TCTAGAGTCT TAGCACTGCT 240
CCCAATTGAG CTTCTACTA ATCAACACTT TCAGAGGCTA CAGGCGACAG CATAAGTATT 300
CGnGTCCCTA CCACCCACTT GGGAGACCTG GAGTCAGTAG TGTCTCCTGT CTCAGCCTG 360
GCCCAGTGCT CACTGTTGCC GGTATTTGGA AGTAAATTAG CAGAAGGCAG ACCT 414

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GAATCCACA AATGAATTTG TGGATGAAAC AAAACATAA nCTCTTGGCT TGCTGAATGT 60
ACCTCTATTC nCATCTCATT TGTGTTTACC TACTTAGATT TCATGAnTTT AAACCTACATT 120
TCTAATAAGG GCTCATAAAT ATTCATACAT GTATTTTTTT TCCTCCAATA CATACTTTGA 180
CAATTGATTA TnTGTTACCT AGCTATGACA AGTTTTTGGC TCTTTATGGC CAGGCTCATT 240
TGGATGATAT CCTTCAGCTT GCTTAAGAGA ATnTAACTT GA 282

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

GTCTTTCCCT CTCCATCACT TTGTCACATA AATTTTTTTT AACTTTGGTA TAACAGGGAC 60
AGATGTGAAC TTTTCAACC AGTTAAACAG CATTTATGAA AAACCTACAG TTAATGGCAT 120
ACTTACTGAT AAAAGACTAT ATACTTCCCA CCTGATATTT AGCCATGATG TAGCTATCTG 180
CTGTGAGCTT TTCTGCTGTT AATGTACTGG AGGTTTTAAC CCATGAAATA AGGCAATAAA 240
AAGACAAACA AAGCACTTGT AACAGCAAGG AAGCAGTAAA ATTCTCTTAA TTCACAGAGG 300

926

ATATGACAGT CTATAAAATT TCAAGAATTT TAACAACTT CTTGAATTCT AGTAACAAAA	360
AGTTACTAGA GTTGAGTTTA ACACAGTTGC AGGTATTTTA AAAGCATAAT CTACTGTGTT	420
TCAATAAATT AGTGGCAAAT TGGTAAGAAA TATGAnTTTA AAAACAATAT AACTTAAAAAT	480
ATCATCAGCA AATCCAAGAT ACTTAGGGnT AAATCTAAAA TAGTATACAC TGnAACTATA	540
TAAAATGCTA CTGAGATATT AAAGGAGAAT TAAATAAATA AGG	583

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

TGGnCAATAC AGCTATTTGG GGAGGGATTC AGTGGATGAA AAAGATCTCT CTCACTCTAA	60
CTTTCAAATA AATAAATATT TTTAAAAATC AAATAGAATT TCTTCATTCT TTTCAATTGT	120
TTAATTCCTA AAATGCCTG CTTTCATGAT ATGATTGGTA ATGTAATTGA AGAAAAATCA	180
TAGGACTGTA CCTGCCCACA ACAATGTGCC TAGCCACCTA CCCATCCTGG CAAACTTGCC	240
ATGAAATCTC TGGCCCAGGG GAGTAAAGTG CTTATATTAA TAGCAATCAG ATTTCTTTTG	300
GAGATATTAC TCTTCAAATT CACAAAAATT ATTTGATGGG GAGGCATGGG ATGGAAGGAA	360
ATGATGTGGG AAGATAATCT CAATGAAGCT GATGTTGAGC TATACCAAAG TGTGATGGGG	420
ATCAAGTAGT GAATATGCCA GGGGGTAGCA CCCACCATG nCTCCATTTT GCCATTGGGG	480
nACCTTTTGG AGTAAGGAAG GAAGCCATGG TGGTGGGGAG CCAGGGG	527

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

TTCAGTCTA GCATGATGCA GACTTACTGG AGGTATTAAT TTCATACTG TTTGAAGACA	60
GAGTGCATTG ATTTCTATTT GTCAAGAATT TTTTCAGAAA GAATATTGAA TTCTATCAAC	120
TGCATATTTT TGGACTTATG GAATGATTAT ATGGATTTC TCCTTTGCAG TTATATTATT	180

927

GGATTTGTTA ATGTAAATC ATCTTTACAC TTTTAGAATA AAGTCTACTT GGCCAAGGAA 240
 CACCCTTTTA AAGTGCTGCT AAGTATGTAT GCTAATATTT TATTTAAGTT TTAGAAAATG 300
 CCAACGCCCA AAGTTAGCAC AGTGGCAGTG CCATGGCTCC GGACAGTTGG ATTATGTAGA 360
 ATGGATCTTT TGCCAGTAGA TGGGATCATA GGAACAGGGC TCAGCCCCCTC AGGCAGGGAA 420
 CTGGTTAAAG CCACCCAGGG TGGATTTCTG TTTTCATGAA GATCTAGCAA ACTTCTCTCT 480
 GTTCTGGCA CTAAGTGAnA CTAGGAACTG TGGGACATTT TATATGAAAC AAATGTAAGA 540
 AGACCAAAGG AGACAGAGAA GAGAGCAGCA GAGCCCTnGG AGCC 584

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

TAGAATGGAA GTAAAGATAA CCTGCTAGGA GGCTATTGCA GTGGTACAAG TAGATGACTA 60
 TAGTGGAAAC AAGCAAGTTG GCCTCCAAGT TCTTCTGATC ATGTACTCCA TTTCTAAGAC 120
 AAATTTGCTG TTTTACCTCC AAATTAAGTA CACTTATGTA TTCCTATTTA ACCAATACAC 180
 ATGCTATATA TAAAATTAAA ATGTTGAGAT TTTAAAGGGA CAAAATAAAA ATGAAGTAAG 240
 CTTTATAGT CATTTTTTAAA TTCCTCTTAT TACTGAAAAC AAAAGCATTG TTACACAAGA 300
 AAATATAGTG CTTCAAAGGT CTGACACTAG ATGGACTTAC TCTGACATTT GGGTCCTTCT 360
 GATGCCACAG TCACACAAAA GATACAATCA ACTACGTACC CAACTAAGCA CTAGCATATA 420
 ATTTCTTTCT TTTATTGCAT TTCCACAACC AAATATTTGG GCACTCTTGG ACATAAAGGA 480
 ATATTTTCTT CnTTTGGA TAAncCTTTA CCAGGGAATT CCACCCCA 528

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CTTGGGAAAG ACTGGGGACT GGATAGGGGA TACTGTAAGA TCGCTGTGAG CTGCTTCCCT 60

928

AGGGGCCACC AAGCATCACG GTCTAGAGAG ACAGAGAAGG CCAGGCTTGG CCCGAACATT	120
TACAGGCCCA AAGATTGTTT TCTATTCCCA CCCCAGTCCT GTCCTACATC ACAGATTGGA	180
CACCCAGCTC CTATGTCCAA ACCTCATCTA TTCTCCAAC AGCTGCCCTT AGCCACAGCT	240
CGGGTCTGGG CATTGGGTCT CTCTGGGAGG ATGGACTGGA GCAGGGGCCG GCGTGGGCCC	300
TGGAAGCGGT TTGGGGACTC TTGGACAGGG AATTCCAAGG TCGTGGGGAC CCACAGCTTC	360
TGTC TGGAAG ATGAGCTGTA GGCTGAGTGG AAAGTCCCTT GTCCCTGAGG GTTTC'TTTGT	420
CCCTTGGGGA GTGGCATGGT GAGAAGGGGG CCAGAGCAGG AACCCAGTTA CCTTGAGCCT	480
CAGGGCAATC CCAGAAATGG GCTCCTTGAG CTGCACCTGA TGCTCTGACA TCAAAAGAAA	540
TACAAATAAG AGTGA ACTCC AGGAGGGCAG GCCTCTGACA T	581

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

TGGTTTAGTC TTTTCAACAA AAACAAAGTC AAAGGTTGAA GAGCATCGCC ATCACTAGCG	60
GTCAAGTTTC TCCGGTCGGA AAGGCCTGGA CAGGGATAGA TGGATAGGAC CTTCAGCTTC	120
ACCCTGGCTG GAGATGGCTG GGCATGGGCG AGCAGAACCA AACTGGCCGT TATTAGGCAG	180
CTGCTCTGTG CCTGGCCCTG GACGTGGCAG TGGAGATGAA CTGCAAAGAT GGGTAGCAGA	240
CACCAAGTTG TCAAAGAGTG GTACCAGGAC AACTCCCCAG GAAGTCAGGG AGTGAGTGGG	300
CGAGGGGCTT CCTGGAGGAG GTGGGGGAAC AGGGGATGGA GCCAGCCCCG ACGCAGAGAG	360
AAGGCCATCT GTGGAATGCA GAACCAAGTC CAGCACACCC TCCTGACTCC AAGGGAAGAA	420
GCTGGCAGGA GACAGGGTGA GAAGCAGGTT GGCTGGGACA ATGCAAAGTC TTCAAAGCAG	480
GCTTCAGACT TGAGGTCATA TTTTGG	506

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

CGAAAAAGCT GATCTGAAAA GGCTACATAC TATATGATTT CAACACTGTA ACATTTTGGG	60
AAAGGCCAAT CTGTGGATAG AAGACAGGTT GTCAAGAGTT TGGGGAGAGA GGAAAGAACA	120
AGCAGAACAC AGAGGATTTT TAGGGCAGTG AACTATTCT GATGAGAGTA TAATGGCAGA	180
CTTATGTCCT TACACATCTG CCAAACCCC ACAGACTGCA CAATATCAAG AATGAATTCA	240
AATGTAGACC ATGGAAGATC ACGATCTATC AACGTAGGTT CCTCCACTGT AACACATCAC	300
TCTGTTAACA GGCTGTTGGC AGTAGGGGGA AGCATTTGGG TGTGAAGGCT ATGAGAATTC	360
TGCACTTTCT ACTCAATTTT ACTTGGAAC TCAAACTGTT CTAAAAAATA TGGTCTATTA	420
AAAACAGTTT TTAAAGGGAC CAGCATGGTG ACATAGCAGG TAAAACCACA CATGTGATGC	480
CAGCAGAGGA TGGCCCAAGC ATTTGGGCCC CTACTACCAA TGCAGGAGAT nCAAACGAAG	540
CTCTGGCTC CTAGCTTCGG AATGGCTCAG CGTTGGCCAC TCGGTCATC TAGGGAAGTG	600
ACCAAGTAAA TGGGAGATCT CCTGTGTnT CTCT	634

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

ATTTGTGCAC ACAAGATGTC CGCTGCTCCT AAGGGTGCAA ATAATAGCTT TGCCAATATG	60
AAAGCAAAAC ATAATTACTC AACAATAAAC AACTGTACA CTGGTAACAG CTGCTATCAA	120
CAGCATGTTG GAAGCCAAAA CAAAGGAAGT ATTACAGGAT TTTTTTTAAA CCCCTGCCTA	180
TCATTCTCAC GGAGGTAAAG TTAGTTTTTG TTTCTGTCAC AGCAAGTGTG ACTAAGCAAA	240
AAGTATTTTA CTCAGTTAAT ATTTCACTCT TGCTTTTAGG TCAGAAAAGA AGCTTGGCCT	300
CATTTTGTCT AGCCAGAAAG TGGGAGGATG AATTTTAAAG AATTACTTAG AAGATCTTTA	360
AGAAAAATCT GTTATATTAA GCATGTAGGG ATTTnATACT TTTCTACCTG GAATATTGCA	420
GAACTACCTT TGATAACTGC TTTACTCTGG CTGT	454

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

TGAGTGATGG CAGGAGCGGC CCTCTCTCCC TCCCATCCCC CAGATGTCAT CTGTCTACAC	60
TGCGGACACC GAGnCAGGCT GCGCTGGCCA CGTGCGCAGG ACAGAGCACT CAACAGCTGC	120
CGTGGGCTGA GGGAGGCTCT GCTTCTCTCC ATACGGGGTC TTTCCTCATT CCTTCACCCA	180
ATGGGGCTAT GCCAATGAGA GTGATGGTGC CCCAGCGGA CCTGGGACAA CGAGGGGTTG	240
GTAGACACAA CGGGGCTCCA TACACCAGAC CCCCACTTCT ACCCTGCCTG GTGTCAATCT	300
CAAAATTCAA AATTCTCCCC AAGAAGAGAA AGAGTAGGAA AAAGCAGCAA AACAAGTACT	360
TCCACTTGTC AGCATCCCTG AGTAGACAGT GCTGCCGTCA TCAACCAACA CAGCCAAGGT	420
CGGTCCGGTC AGAGAAGGGC TCCCCGAGG	450

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

CTGnAGCTGT GGCGCCACTT AAGCCCAACT TTAAATCAAT AAGATTATGT CACTTGCCCA	60
GAAAAACAAT ACAAACAGAA GTGTTACTCT AGGATAATGT CACAATACTC TCTAATAAAC	120
CTTCCATTCA AGGTTCTTTG CACAGGATGA AGTCACACAA CTGAGTGTTT TCAAAATATA	180
AGCTACTTGA CTTTATGCCT ATTTGCTAAT GTGTGTTTGT GTGTTAAAGT CTAATCCTAG	240
AATGCTCTC ACTTGACAAC AGGTTTGGGT AGAGGGGAAA AGGAAAGAAC TTAAATCCTC	300
AATTGTTTCA AATTTTACTT ACATCTAATG AAAGAAAGTA ATGTATGTGA CTATCAAAAC	360
TGGTTTAACT GTTTACAGTA TGCTTAGGCC ACAACATCAT TTATTCCTT GTTATATCn	420
TTACATTAA AAAGCTCCAT TTTTCCAAC TCGTGTTAGG CAAACTGCTC CACTATTATG	480
ATAACAACAG TnATCATAGT TAGGATAACA AGAGTTATAA TTTTGATATG ATAnGGATAA	540
CAACAGTTAT AATTT	555

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

```
AAATACTGGG ATTCATGAGT TTGATTAATG AAGAAAGATT ATTAATTTTG TGGTTTCCAA      60
AAATATGTAA GTAGAAACAA GGTCATTTAT TGTACTCAA TACAAGAATC CCTATGATTG      120
AATGACACAG ATCAGAAATA AGCCTAGGAG ACATACTAAT AACTGTCTCT GCATCTGAAT      180
AAATGAACTG TTAGTAATTA GAATTCATTA ACCACATAGG CTAATGGATG GAATAACACA      240
ATTTTACTGC TGTTTTAAAG TTTTGGTCC TCATTTATTC AAATGGCTCT ACTAAGGACA      300
ACACTGATGG AGTACTTTGA CCTTTGTAC ATCATTCTT TCCAAGGTGA AATTTCACTT      360
GTTCTCTTTC TCATTAAGGT TCTGCTTGAA AATGATTCAT GCTTGGCCGG ACGCTGACAG      420
GTCACTAGGG CTAATCCTCC GCCTGCGGCT CCGGCACCCC AGGTTC      466
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(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

```
AATCTTATTT GTATACAACC AGCATAATTT TGTTATTGAA ATTTGAAAGA AAAGGAAAAT      60
AGCAGGTCAG TCTACTTATA TGAACATAGA TGAAAAAATA TAAATAGAAT ATTCATTAAT      120
ATTCATTTGC AGACAATATC TAGTGAAATA TGAAAAGAAT CATGACCAAG TGGGTTTATC      180
TGAGAAATTT AAGTTGATCT AGTATGTGAA AATTAACATT CACTGTATTA ACAAATAAA      240
AAACCAAATG ATCATTTCAG TAGCTGCGTA AATCTTTTAT TTAAATTGTA TTCAACACCC      300
ATTAATGATA TAAAAAGCTT TAACAACTT GTGATAGAAA GATACTTCTT ATATGATAAG      360
GGCTTTTTTT TAAATAATGG AGTGTAATA TCATCCTGGA TGGTAAAATA CTGAATATTT      420
TCCCTGAGAT TAGGAACGTA TAGGATACTT CACCACCACC AGTAC      465
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(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

CATTTAAGTC GTAACAACT ATTAGCTACA GTAGCACATT ATTAAACAGA TAATGTTTAA	60
CAATTTTATT CACAATTGGG ATTAAATGAG AAAACATCA CATTTTAGCA CCCTAAATAA	120
CAGTTTGGG GATTATTGA ATTGAACTA ATTCTAGCTT TAGAAAGACA TTACTAATTT	180
TCTTTAGAAA ATTGAGGCTA AACTACTTTA GTTCTTCTCT TTTTTTTAAA GGCAGACAAT	240
TCTATAAGAT GATATGGTTA ATTGTATTTA TATTGTAGAT AAAATTATG TATCATCAAC	300
TTGGCAACCG GTCCGAAAT GTCCATGGCA AGTGATTTAC AGTTCAGGA GAGAAAGCGT	360
TCTCTGCCAG GCGGTTGAGC GTTTGGAGG GGGGAAACCT GGGGTTGGG CAGATAAATA	420
TTCAAGCAAGT TTACTTTTGT GTTCCCATTA TTCAGnATTC ACTGCCTGCC AAAGCCTCAA	480
ATTAATCCAA TTAATAATAT CTAAGTAnGT GAACTTACAC AATCCATAAT CTA	533

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

CAGATAATTT AATTAGGCAC TTCAAACGTG CAGTAAGATG GAACTTTCC ATTTGAATAC	60
TTTATGAGTC TAAGAGGGCT TTTGGAGAAA GACTGGGTAA GAGTTTAAAC TAACATAATTT	120
TCAGAAAAAA TGATACCAAC TTCATGCTTA AACAGACTTG TTAAAAAGAC TATCTAGATA	180
TTCAATTATTG TACACCAAAT ATGAAAACAA AATATATCTT GTTTATTTAA ACTCCCTTAC	240
TGGATTATAA TTAAAGTATT ATAATTTACT GATGTACTTC AGTTGTTAAG TTTCTATGGA	300
GACATTTACA TGGTATTTAT AGAACCACAC ATTAGTATGA CTTCAATAAT GTAGCAGATT	360
TAAAGCTGCA TCCCATCTAG ACAAGGATGG TATGATCTCA CTCACATGTG GAATCTTACA	420
AAGGTGATCT CATAGAAGCT GAGAGTAAGA TGGGGGGTTA CCCGACACTG AGGAGA	476

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

GTTTCTGAAA TGAGGCACTG GGGGATGAAA TAGAAACACC ACTGTATCCT TTAAGCCTGC	60
TCTGCAGGTC TCCCCTCTCA ACCACCACTG TGGTTTCCTT CCTCAGGTGG TCGGGATGGC	120
AAGGCGTTGG TTGACTTAAC GACAGCGCGC TGTTCTTCAC TGTGTTCCAT AACTATAGCT	180
TGGAACGTCT TGTCTTCTTT CCAGACTACA AATCTGTATG TTTTGAGCTA TATAGAATTT	240
CAAAGGGCGT TGATAAATAA TGAAAGAAAA CAGAGATTTG GGGTTATTTA ATGTTTGTGA	300
TCTACCACAG ACTTCTCTCA AAAGAGAGCT AGATTTTGTT AAAAATGAAA CTTCTACAGG	360
AAAGAAAAGC TGTCTATATT TCATGAGAAG TTGTCAGAAC ACAAAAAGGA ATAATCTTTT	420
TTTTTTAATC AATCTGATCT GTCACAGAGA AACAGAAAAGA GTATCTCATC TAAnGGGAnT	480
CCCATGAATG CCAAAGTCCC GGGGAAGCCA GGAGACC	517

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

AGTTAGATGT ATTGCTGGGA TATAGGTATG CTTTAACATA TGCAAATAAA TGTACGGGAC	60
ACGCTACAAA GTTAACAGAA TGTAAGGTAA TGTGATATAA TCATCTTAGT TATTTAGTAA	120
AATCATATAA TAGAACTCAG CATTCTTTCA TGATAAAAAC TCCCAGCAAG TTAGGCATAG	180
AGGAAATGTA TCTCAGTATA ATAAAAACAA TATTTTACAA ACCCATGAAT TATCATAATC	240
CATGGTCCAA AAGTGGAAC TTTCTTCCTA AGATCAGGAG CAAGACAAGG ATGCCAACTA	300
TTACCATTTT TATTAAACAT GGTGTTAGAA ATCTTAACCA GAGCAATTAG GCAATAGAAA	360
GGAGTAAAT GAATGAGAAT CTAAAAAGT AAAATTATCT CTCAGGTGGC TGATCTTATA	420
TACAGAAAAT CCTAAATACT AACTAAAAA CCTCATAAAA TTATAAATGA AATCATAAAC	480
AAATCCAGCG TGTTCCTATT CTCTAACAAC AACTGAGAA AAAAGATGAA CA	532

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs

934

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

TAATTTCATh TGGTTTTGAT TTGnACTTGA TATTTTTCAA CTAAATATTT ATTTTTGAAA	60
TAAAATATTT TAAGTTACAT TATAGTCACA TTCTTTATGT GCCACTAAAT AGAGTTCAAC	120
AAATAAAAAG TGAAAATACT GTAGTTTAGC AGAAATATAG GCAAAGCTCT ACAAAAACAA	180
TCAAATGAAA AAGATGTTAC ACAGTAAATT TTTAAATAGT nACAGATCCT TAGAACTGTA	240
GTGGTATATA ATTCTTAACC ATTTGATGTT GAAnACCTTT TTATAATCTG ACCATTTnAA	300
AGTCTTTTGA GAAATGTCTA CTGAAATCCT TTCCTCATTT TTTGTTTGGA nTTTTGGTTT	360
TTGGnTCTCC AGTTTTTATT ACTTCCTTGT ATATTTTATA CAGTTTAACT AGTTTAA	417

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

AAAAATCAGT CTCATTATTT ATTGTCAGAC TTGATGCATT CAATATGGCT GATGTGTGAA	60
GTTGAGAGCA ACACCAGAGC AACCCATTGC TCAATCCCT GTCGTGCTGT CACCTCTTTT	120
CCTATGACTG TCTCAACAGA TGGTCCCAGC TCCTAGCAAA TCTTACCCTA CTTGAGGAAG	180
CAACACGTCT ATTTTTCAGT GACAGTTAAA TTCATGGCCA AGTGCACTGG ATTCCATCTC	240
CTTCTTACTA TCATACCTGT GTCTTCCACT TCTCTCTCAG CCCCTATCTC ATGCTCTCCC	300
TGTAATTTTC TTAGGCTAAT GTAATTCCTT CCTCAATAAA GACCCTCTTG GTCTTTCTGT	360
ATTGGTCTGA CACCACCTCA ACCTGGATCA GTTCTTCATG ATTTCCAAAG TGACACAGTA	420
AAGATACATC AGGATTG	437

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

CTAATGTATA AGCACTCATC AAGCATCCAC TCCCATCATG CTTATCAATA TCCCAGTGGT	60
CAAAGCCAGT TGCATGGCCA AACCCAGGGT CAGAGTTGGA GGGGCTGACA TAAAGGCTTG	120
AATGCTGAGA ATCCCAGTTT ATTGACCACC ACCAACATAA CAGGCTTTAT GAAGAAGTAT	180
TAGGGCAAGG TTCTGAGAAA CCAGAGAGCA TTTTCTTCTT CCTGTTATCA GTTATTTTTT	240
CTTCAGTACC TTATCTGTAG AACACTTGTA AGCCATAGAA GATAAAGTTA CTCATCCAAC	300
ATCAGCATAA ATTCTTAACT CTTTGTAGCTG CTAGAAATAT TTCACAGAGA TAAACCTGTA	360
TCTGGCTTGT AGGAGCTGTG GTCCTATCAG AGAGATGCGT TTGCAAGCAT GCATTACAAG	420
ACAATGTGCA CGACAACAAA CATGTATACC TCAAGTAAAA AG	462

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

GAATnGAGCT CGGATACAGG AATATGTATT GGAAATAAAA GACATGAGCC TCCAGATTAA	60
AAGGACCCTA CCAAATGCTT TTGAACTGTA TTTGTAAAAC ACCCGCCCAA GGCAC TTCAC	120
TATGAAATTT CAGAGACAGC CTACAAGCTT CCAAAGATAA GATAATAAGT ATATTCCTTA	180
GGTGAAATCT TAGATTAGTA TTATGAGTAT ATGACCAGTG GAGCAATAGT TCAGTGATTC	240
TTTACCCAGC TAAACGATCA ATCAAATGAA AGAATATTTT AAATCCTTTT CATCCTTGCA	300
GAATATCAGA AATTGCGCTC TATGCACCCT TTCTTAGAAG ACCACAGGAG GAGGTATTTA	360
CACAAATGGC AGGGCAGAAT AAGAAAGAGG AACTGGAGA TCCCGTAAGT AGAGGTTATT	420
CTTCCAACGA AGAGGCATGC TTTTGAGATA GGAGGTGAAT GGTGTAGAAA TGCATTTTGA	480
CTCAGTAGTT GAAAGTTGAG AGAATTTACA CCTCTGTTTT CTCAGTGGGT GAATGCAGGG	540
nTGCTTACTG TAGTTAGAAG CTTTGAGAAT AGACAGACTT GGGGGACAAG AAAAGGTCT	600
CATAACCTGG GATAAACTA TTGGnCAGTT TGGnATTGGG GGG	643

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

TATACTTCTT CATTGACTCA AGCCACTGAA ATTTTAGAGG TTGTTATTAC AGCACACACA	60
CAGTTTTCCT TGACAGACAC AGATTCAGGT CTAGGAAGGC CATAAATGCC ATATTAAGGA	120
ATTCGAATTG TACTCTGAAG GAGGTGCAGA GATAACATTT TTGAAAGGAG TGACACGATG	180
TACATTTGAG TACAATAACT CTGGATACAA CACATACAGT ATATTGAAAA CAAGGTGACT	240
TTCAACCTTT GGTGTACATA AAAATCCCCC ATGAAGAACG GTAGTCACAT TCCAATTCCT	300
ACATATTACA CACTCTATAA AGAAGAAAAT ATTTATCCTC TGGGGAAAAA AGTTACCCAG	360
GAATCTTCA AGATGCAATG CTCTGGGCCA GGATATCTTC AGATATCCTG AATCAGCATC	420
TCTAGAGGTG GGGTTTATGC ACAGTAACTG AAGGACAAG CTGAGTTCAG AGGTAACCAA	480
ATTCACATGC TTGTGGTTCA AATAATCATT CnCCCTCATG GAT	523

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

AGAAAAAAAA ATACTGCAAA TATAAAGGAA GAAGGAAGCA AAATGTAGAA ACTGATGAAA	60
TAAGAAATGT ACAGCGGTAC AGCTTACCCA GGTATAATCA ACACAGTCAA CACCAAACCT	120
GGAAAGAATC TGAAAGTGTG AGAGCAAAGC ACGAACAAAG ACAGCCAATG TCAGTAATGT	180
AAAAGTTGCT ATCATTCAT TATCCACAG ATAAGGAGAG GACATTATGA AAAAATTTAT	240
GCCATTTGAA AATATAGATG AAATAAAAAA GTCCCTAAAA TAATACAAAT CACCAAACCT	300
ACAAAGGAGA AAAGACATAG GGCTGTGACT CTAAAGATA TTAAAGTCT TACATACAAA	360
AATATTCCAG GCCAAGATTA CCTCCTCTGA GTTCTAAGAA ATGTTGAAAG AACAAATAAC	420
ACCCACCTTA CACAGACTCT TCTCAAGAGT AGACCTCCTA CTGAGGTCAG TGTAACCCnG	480
GAACCCGGCC nGnGCAnGGA CGTTGTAAAA CAGGAAATTT ACAGGGCTTG ATTTTCATAAT	540
CAGAATGAGA AAATCTTAAA ATAGCAAGAT ACAGGAAATA ATATCATAAT CA	592

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TTGTGTTTTC CACTTGCTTC CGAGTTGCAC TGTTTCAGATA TTTTAAATGT CCATGTGACG	60
CAAGGCTCCT AGAAAAGTTC ATGGAAATGG ATTTTAAAC ATTGACTTGG GCAAAACTG	120
TTTGGAATCC ACCTATGCAG ATAAGGGGTC TTCAGAAAGT TCCTGGGAAA ATAGGTAGGA	180
AGAAAAGTT ATGCATGGCG TTCCAAAACA TTCTTTTTCG ACCAGAATGA GCTCAGTTTT	240
TGACTCCTAT TTCCATGCAT TTCTTAGTCT CTCTGTATTT TCTCCATTT TCCTTTGCCT	300
TGAAAACCC TAGTGTAGAG TGCATTTCTT GTCTGGAGAC ACAGACACAA TCTTTCTCTT	360
TGAAAACCG TGTGTTGAAA GAGTGAGTTG ATGGGGCCGG CGCTGTGGTG CAGCGGCTTA	420
AAGCCCCGGC CTGnAAGGCA GGCATCCCAT ACGGGCCGG CTTCGAGTCC GGGCGCCGCT	480
TCGAGTCCCG GGCTGGCTCC TTTTCTGATC CAGCCCTCTG GCTATGGCCT GGGAAAGCAG	540
TAGAACACAG CCCAAGTCCT TGGGGCCCCCT GGCACCTGCA TG	582

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GTAAGTCCA ATACCCAGTC CTCAGCAAGA TTCCAGTTCA GTTGTTTCAGT TATCAGTGGT	60
GATTTTAATG CTCCGCAAGT GATTCTAACT GCAACCAGCG ATGAGAAGTC CTTTAGGTTT	120
CCCTGGAGCT AATAGCTGTC CTTATTTCTG AAATCAGTCT TAGGATTTCA GTGACATGCA	180
AATTAAAGCA TCTTAAATAC GGACCGTTTT CTTTGAGTGC AATGCAAGGT TCAGTGTTTA	240
AATTTCTTT AATTAGAACA ACTAGGAAAC TTAAAATCTC ACTTCCTGGC AAAAGAATTA	300
GGCTTGCTCA TTTATTTGAG AAAAAGATTA TGTGCCTGCC CAACCATCAA TCCTAATTCT	360
GAAGACCTTG CACTGnAGGG ATGTCAAAG AGGAGCTGGT GACTAACAGG AGGGACTGAG	420

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GGTAGGGACT TTGnAATATG GTGAGGAAAA AAAAAATCAA TGCCTCACTT ATCCTTGGGC 480
AACAAATAGA TATTAATGGT TTTAACAACCTG ACCAGTTGGG ATATTATTTT GTTGCCTACA 540
GCTGAGTTTA AGATCCATAA TTTCACATAG TTGTTCCAGG An 582

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

CAGnAGCGGG CGCnGGCGCC CCCAGCCCTC CTTCCACCCT TGGAGCTCCC AGGCTGCCTG 60
GCAAACCCTC TCCTCCCTCC CTGCGCCCCA CCCCACCTC ACTTCCTCTT TTCTGGTCCT 120
CAAAGGTACC CAGCTGCTCC AACCTCGGGG CCTCTGTGTC CGCTGTTCCC TCTGCCTGTA 180
ACACCCTTCC CAGGCACGCT GCCAGGCTGA GTCCTTCTCC AGCCGGGGCC TCCTCCCTGG 240
AGCTGnnCCG CCCTGGCCCT CCCTGGTTAA TCAGCGAnnC CCACCCCTTC ACCCCCGCCC 300
CAAGTCGCAC CACCCTGCTG GACTTCCTCT CTCCCAAACC GTCTTGTTTG TGAACCTGTT 360
GTGGTCACAG CTGTGGnnCC GTGCTC 386

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

AATGAAATGG AGTAGAGAAG AGACTTTTCA GCCCAGCAGG GTCTCCCTCC TGTGCGGACG 60
TTGTTCTCGG GGATCTGCGA CGGGAGCTGT GGGCACTCGG AGCCGAGACG CAAAATGAGG 120
CTCACAGACC AGAAAAGGGT GCAAGCCACC GTCGCTGGCA GCCGCGGGCC TGGCTCGCCT 180
CGCTGGCCCT TCCTAAGGCC CCGCCTCTGC GTCCCCCAGG GATGGAAAGG GTGCAGACCA 240
CCGAGCTCCG AGATTGCGAG AAAGAAGCGG CTTGGGGAGG CCCC GCGGGG AGGCTGGGGG 300
ACTTCCTGTT CCGGTCTACG CCAGGCGCAG CCAACACTCG CAGGAGCTCA GCAGCCCCCA 360
CCTGGTGACA GCCTGGGTGG GGCAGGGAGC CCCACCACCA GCCGCTGCTT GCTGTCCCCC 420

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ATCCTCCCCA CACACAGGGG ACAGCTCCTA GCTGGCTGCT GAGGGTTGGG GTGGGGTGGG 480
CATGGTGGGG TGGGGAGAAG GCAGCCCCGG GCTCTGGTGA CCTGCCCAnG ACCTGCCCCG 540
AAGCCCTCTG TACACTGCCA CTGGTTGAAC TCATCACAAG TTCCGCCCAG AGCCCTGCAC 600
TAGGCACTGT GTGTTGAGTT CATGCGACCT GCACCACAAG CTGCACGCGC ATGGGCACAT 660
GCG 663

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

TGCAGGATGT CCAGCGTAAn AAAAGGGTTG GGGGGATAAT TGTACCTCCA TGACAGGCTT 60
CACAAACTCC AGGAAGACGG GAAGGCCTAA TTCTTAGAAA ACGAAACTTA GTATATACTT 120
CCTGAAATTA ATGGTCTCCT ACTTCCTTGT GTGACCACTT CCTTCTGAGA CGCATAGTCC 180
TGGACTGCTG AGATGCACCA ATAAATGCT CAAATTTAGG TAATTGACAT ATAAAGAATA 240
AGGAACTAGC ATATGTGCAT AATGACGAAT ATACTTGTTT ACTCAAGTGT ATAACAAC TC 300
GGAGAAGGGG AGAGGCGGGG CTTCTCACCC CCGGCAC TGn CACTATGTTT TATGTGTCGG 360
TGGGAGCCCC AGCTAGCTGG TAATAAAACA ATAAATCTCT TGGCCCTTGG CATCTGTGAC 420
TGTCTTTTGT GGGTTAATGG GAAAGATCTC AGATCCCAT ATTCAACACT ACATAGGAAA 480
CCTGGATTGA GTTCTCAATT CCTGGGCCTT GGTACTAAC ATTTGAGGGA GTGAGCCAGA 540
GAG 543

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CTGGAATATT TCCCCTAAGT TAGGTATGGC ATTTTGT TTG GGAACAAATC AGAATTTGTT 60
TCTTCAATAT TAAGTTATCA TTTCACCTAA ACTACAAGTT GACTTCCTGA ATTGAGGTCT 120

940

AAAGCTCTTC AACTCTGTAT ATTTAAAGAA GTTTATTAGA TAAAGAAGAG ATTTATTTGT	180
AATTTTAAGT GCTTTAGAAG TAGGTTCTAT CTTGTTCTGT TTATCTTTGT TGTATCACAT	240
GCTATGAATA TTTTAAATGC ATATACTAGT GAATAAGTTA AAGAAAAAAA ATCAGTGAAT	300
GACTAAGGCC TATCCGCCTG ACAAGTTTTC CATCCATTCA TTTCTCTAAA GCATTTCCCA	360
GTCAACCTGA AGTTTTCTTT CTGAAGTCC CCTACAAAA GGCAAGGAAT GGAAGAAATG	420
AGAGGAGTGT CTCCAGGGAT GGCAGAGCTT TGGCCAGCAT TGGGCGTAA GATGAATCTG	480
CTGTCTGTTG TGGGGGAGGA TTGAGTCCTG CTCATCCTCT ATGCAACCCT AGTCCAGCTT	540
TCAGGCGTGG nTAACCCCTT TTCAGAATGT AGCCAGCCCA GGCC	584

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

AGGCCCCACC TCCAAATAAC CTAGGAATCT GGGGACTCAG TTTGCAAAAT GTTAGCATCC	60
AATGGTTTGC TTCAGAAATG CCTGAAACAG CTGGTGTACG GCTAGGTTAA AGCCAGGATC	120
CAGGAACGCA ACCCTGGTCT CACATGTGGG CAGCAGATAC CCAACTACGT GAGCCATCAC	180
CTGCTGCCTC CAGGCTGTGC ATTAGTAGGA ATCTGGAATT AGGAGCAGAG CCACTCTTGA	240
ACCAGGCACT CTGATATGGA ACACGGACAT CCCAACCAGT GTCCTAACGG CCGGGCCAAG	300
TGCCTACACA TGTCTCATT TTGATGCAGG TTTTTTTTTC ACTCCTGGAT ATTGGTTTTA	360
AATCTTTATC CCTCAATTCA AGCAGCTCAT GGAAATATAG CATTTGAAGA CGTACCAGGA	420
GAACGCACAG CTGACCAGCC AGAGCTGAAA TGTGCATGTT GAAGACTGGA ATGGCTGTGG	480
TATCAACAGA CTGCAAGCTG GAGTCCACAG TAGATCCTCT GCATTTCTCA CTCACTGGGA	540

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

941

TGCAGGTAA GAAAGTACTT TTCAAGTTAC TTATCTGAAA ATACATCTGT CTAGAGAGCC	60
TCAAGATAAA AGAAATGTTG GCAAATTTTT AATAGAACAC AATAATATGG AAAAGCCTAC	120
AGCACTTCCT CTCCAAACTC CTACAAAATG TCAATGGTGT AGTCAGCAAG TAGTCAGAAT	180
TCTGTGAAAA CCATCGTAGG CATAAGAGAC TCTTAAGAAT AGGAAAAAAT ACCCACAGAT	240
GCTTAATTGG TGAAAACGTG CTGTAAAGTA TTTCTGAACA AACTTTTAGG AGGCTGAAGT	300
TCCTTGTGGA AAGCCCTCAG GCACCTGTGG TGAACCTGCA GTGGAAGTTA ACCCCAGGCG	360
GAAAAATATGC TTCTTCACA CTATGGTCAA AGCAACGAGG GTGGAGGGCA GGGACATCTG	420
GACATTAGCA AAGATTCTGC TTTGAGGGAC AACTGTCATA AGAGCTCCAG GCCTACGTCA	480
AAAGTGCTC AGGAGAGGGG TGGGTGAACA AGCT	514

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

ATAATGAGCA TTTTCCATGA CGTTTTGTGA GACGCCCTCA TGCACAGGAT TCCTGGGAGC	60
TGGTCCGTGG GGGCAGTGTG AACCAGTCCC ATCCTATGCC TCAGAGGTGA TTTTTTCACG	120
GAAATCTGTG GAGTGCTGCT CCCAGGACTT GTAGGCATCC ATAATGGTAT AGGAAGGCTT	180
GTCTTTGGT CCGTAATGCC TTCAGTCCCG TGGCCTCCT CAGATTCTGA CGGCGCGCAC	240
CCATCGTGTC GGGGACTGGC TGGACTGGAG CATCTGCCAG AGGATCTCGG TGATCACTTA	300
GCATGAGTGA ATTGACATGG CTGTTGTAGA GCTTTTGGGC AGCCATTTTA ACGTTGTGTA	360
GATAGGTAC CCCCAACACT GGGAAGTTGC TACTTCATCA CGGTGTTTAA GGTCCTGAG	420
AAGTGCCGTA GTCGCCTGTG GTTCTCTGAT CTCCAGAATG GATAAGAAGT CAGCCCTTAA	480
AATGTCCCCA AAGCTTCAGC CATGTTAATG AAGCCGGATG ATTTACAAGT ATTATTGGnA	540
CTTTTAAACC AGCCTGGCTG CTGGTATACA TATAATTCTG ATCTTACTTT ATTAAATTC	600
TCAGTATGTA CCTTATGAAG ACATTTTAA TTG	633

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 514 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

AAAAAAAAAA AAAAAAGTAA TGACTTCTAA TCTCCATAAT TAGGTCATGG TTTGGCCTTT	60
ACACACTCCC ACTTCTTTTG TCAACTTCTA GCAAGAACAT CACAAATTTT AGAAACTGGT	120
ATTTAATTTT TTCATGGACT TAATGATTCT CCATCCAGCC CTAATGATCT CAGTAATTAG	180
TACACTAATC TAATACACTC TTTTGTAAAT AAGAAAATCA CTGGGAATTA AAAC TAGCTT	240
CCTATTTGAA TGAACATCCA TAATCATGCT TCTAGACTTT AGACATTTAC CTGATCCATC	300
TGTTTTCACA GGAAAACGAC CACTAAACAT AGACGCCAGC ATAGAGTCTT TGAAACGACA	360
CAAGGACTCA CGCCGGGCTG TGTACGTGCA GCCACCCACG TTCAGCCGGA GAATATCTAG	420
CACCTCTGTT TCTGCCTTGG GGCCTGCCAT TGCTGCCTCC CAGCGTTCGC nGAAACCTCA	480
AGGCAAGCAG TCCTGGTCCC CCTCTGTGAA AACA	514

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

TAnAGTGCAT GTTTCCTGTG GGCCATATTA AAATCGCTTC ACTACATTGT CTCACATAAT	60
CCTTTTCCGA TAGGTCACTG GGCCTTAGGG GCCTTAAATA AATTGTCCAA AGTCAAACGA	120
GATAGCAAGA GGCAAATCTG GGCTTTGCAC TGATGCTAAC ACTTTCTAAA GTCCACGTTG	180
CATGCCTGGG TGATGCTTGA ATGCTCCTCT GCACATTTTG CTTTAACTC TGCTATTACC	240
TTCTTGGTAT TGTATCATGA TTTATTGGTG GGTGAGTCTT GTCTACCCCA GTAAATTGTA	300
ACCTTCTCAA GGACAGGGAA TAAGTTATTC AAGCCTATAT CCCTAGCACT TAGCAAATTG	360
TCTGGCACAT AACAGAGCCT CAGTAAATGC TTGTGGCCTG AATAAATAAA AGCCTTGAGA	420
GAGATGGTCA GGGAAAAGCA GACAGAGTAA TCTAGATTGC AGTTTGAACA AAACACCTCC	480
TTTCCTATGG nCCTGATTAG GGAGGTGTCT GCTGGGCATG GAAGGCAGAT GGGTGAAGGA	540
GCAGGGACAG CCATGCCTTT CCCTGGTTCT CTGGAAATCC GGCT	584

(2) INFORMATION FOR SEQ ID NO: 366:

943

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

CAAGTGATCC AAGCAAACG AAGGACATTT GCATTACCCC AATTTTCTGA ACCAATCTGT	60
ATTGGTTTAC TTTAATTAAC AACATAAAGG CTTGTATACA TAGAATTTAC TCTCATTTTT	120
ATAAGACCAC TCTAGCTGGA AAGCAAGAAC ATGAATACAA CATAGGTCTT ACATCATTTA	180
CAACATTTTA ATGCATTTTA CATAATTTGA ATTGACTTAA AAAGCTGTTA CTTTATCAAA	240
TTTAGAGTCT TCTCCTTTGA GAATTCCAGG GATCCTACTG GAAGCCTCAA AATTGGAAGA	300
CTCAGTTTAG GGCTTAAACT ATCAGAGAGT CAAACTATTT AGCCAAAAAT TAGTATGTTT	360
AACCTTGAAA GGAACGCTG AGAGCCGAGA GCCAAGAGCC GCCATAAAAA AATGGCCTTA	420
ATGAACAGT CCTGGGAAAT GGGGAGTAAA CTAAGTTCAC AG	462

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 614 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

CTTAACGTAA TCCTATTTGT CTGAATTTCC CATTACATTA AGAATAATAT CTCATCGATT	60
CAAGCATTA TATGAGTTA AATAAAATAT CTGACAAGTG TTTATATCTG TGAGAGTCAG	120
AATTCTATCC TTTTTTAAAA ATTAGCTCAG GAAAGTTCTA TGATTATTAT CATCTTATAA	180
CACAAGAAAC TGAAACTTGA AAAATTTAAG TGTCTTGCCC AGGTTGTTTA AACTGCATGG	240
CACTGGACTA TGCTACAAAT TAGATTTCTT GGTTTTTCTA CATTGTTATC TCAAGTATCA	300
GTGACATCAA GAAACACAGA AATGTGCTAG AAAAGCTTTA AAAACATTAC AGCCTATAGA	360
ACTATCATAT AATTTAATTA GTGAAGACAT CTTTACCCAA CTAATTAACA AATGAGATGG	420
CTTTTCAAAA AAAAGTTAAG TTTAATTTTC AGTTCAAATA AATGAATATA TGATGTATGG	480
GGGTGTGGAG GCAAAAGTTC CTGAATCCTA ATTCCAAAAC AGAGTTAAAA AAAGAGGACC	540
CTGGCAACAA TTTTGGnCCC ACAATCATTT GTGGCCCATT ATGTGCTGTA AGAAATACTT	600

ACTGAAGCTT TTTT

614

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ACCAATAGAG CTCTGACTAT CACAATCACC CTGGAATCCC AGCCTTGGA AGACTCATTC	60
TTCCACAACC CCATGGCTGC AGAGATGTGA AGAAAACAGC AACCCACAGA TTAGAGGCCC	120
AGCCTGACTG TGACATGCCA CTCGTGCTGA CATTCCACCA GCCAGGGTAA ATCACACAGC	180
TGTACCTGCA TTCTGTAAAG TGTGGATGTA TAATCTTTCT ACAGAAAATG ATATTCTGAT	240
AGTGGTGAC AATAGAAGTC CACCACAGGG ACAAGCCTCA GGAAAGGACT CAGGTAAAC	300
CTCAGCCACG TGGAATCTAA GGTCTGCGC ACATTTCCAA GTTAAGGAGG AGTCAGACAA	360
ATATGGCTGT ATCTGTAGGG TGGGAGTCAC ATAAAACAGG TGGAAATAAG TTCAAGAAGC	420
CAGTGGTAAA AATCAATCAT GGTAATAAGA GTAAGAACAC CTACCACCTA TTTAACATCC	480
ACCCTTTGA GTCAGACATT TTACATACAT GTTATTCTCA TCATACTTA CCATAAATTA	540
TTGCATTCCC TTATATAATC TATGCATCAT TTTATCTACA TAAGTATTCT ATGAGTTAAA	600
TGTTTCTGCC ATTGTATTAC AGAAGTGAGA CTGGGAGTCA GATTACATCA CTTAACCAG	660
GTCAAAGGC AAGAAGAAGG CAGGGAGTTG AACCAGTTCT G	701

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

TGCCCTATTT CTGTAGCTGG AAGGCACTCC ATGATGTCCA GATTAACTG TTCTTTCTCA	60
TAGTTGGAAT ATTTTAGTG ATGTAGACA AATCACACTT TAATTGAAC TCTAGAAGGC	120
AAGAGGCTCA CATTAAGTGA ACACGTACAG CAGACATGAA GGGGAAGAGT GTCTTCGTTA	180
TGGGTGTGCA GTTTGGCAGA AATGATGCCC TGAGTGCATG TTAAATAGTC TAGCAAAGTG	240

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AAATCCCACA GCTCAGCTGT GAAGTCAGTG AATATAGCAA TCTGTGTGTG GCAGAAGCCT	300
TCACAGCTGC TCCTCCATGG TGCACTCTGA CTTGGGGATT TGTTTTGTGTT ATACAGCTCA	360
CTGGGCTCTC CATAAGGCAT GAAAGAGAAA AGTTTGACTG ATTTGCAGCA AATAACTCTT	420
TAGACTGCTT TCTATTGCAT TGGAAGCCTG CTTTAGAGTG TGTAGATGCT AAATAAATGG	480
TAAGTGTCT ATGTTTTATT TTTATCCCTG GCTTCAGCAA CTTACATTTA TAGCATAATT	540
TTTGATTTCT GCCTGCATTA GAGCAGGTAG GGAAATATAA TTAAGAGCAC ATTTGATTCT	600
AACCTGCTCC TATGG	615

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TGCGGATCAn TnCCCAGCCC CGTATCAGAG AATCGGTTGT TAAATGTTTA CCGACACACC	60
ACTGGCTTTG GTTATCATTT TCTTACTTCT TTCCTTATTA GTTGCACTAG TTTGCATACC	120
CATCAATGAT ATGATGGGTC TTTTTTTTGA GTTATAATTC ATTATTTTCT TTTAAAATTA	180
AAGTAGTAGT CATCCTTCCA TACAAGGAAA GGATTGGAAG GAAAAAATC ATAATATTCA	240
AAGATAGGCT TTTGGTGAAC AAAGCAAGTA TGGACTTTGA GCTACATGAG ATCTTCAGAA	300
AGTGCTCAGA ATATATTTTT TTCTACAAAG AAACCTTTTA TTTAAGGAAG ATAAACTTCA	360
TACATTTTCA AAGTACGATT TTAGGGAATA TAGTGATCTT CACACCATAC CTGCCCTTCC	420
AACCACTCTC CCTGGCCTTC TCCGTCTCCC TCTCCCGTCC CCTGnCCCAT TCAACATGGA	480
AGATCCATTT CAATTAACTT TATAAACAAA AGGACCAACT CTA	523

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

ATTAGTAGCA TGATAAGTCT GCCAAAATTA ATTTAAATAA ACTAAAATAA TTAATTCTCA	60
-------------------------------------------------------------------	----

946

GTAAATATGA AGCATCTACT GAATAAAAAA TCGTGGTTAA CAACACATAC TTCCTATGCT 120
TGTGAAACTT ACAATCTACT CAGGTGGGGT AAGGCCAGAA TATATGCACA ATACTAACGG 180
ATTGGGGGTA GGGAAAAAAA TCTGTCCAAG GAAGGGACAA ATCTCAGAGA TACAGAGTAG 240
GGAAAAGCCA GGAAAGAGCA TGTACCAAGT CCTAAAACAG GAAGGGACAG AAATCCTGGA 300
GACGACAGTT GGGATGGCTG GAGAATGCAC CACCCTAAG GCAACAGGAA TCATTGCGGC 360
GGGGGTGGGA AGCTTTATTC TGCCAAGGGC CATTTGGATA TTTATAACAT CATCCACAGG 420
CCCTACAAAA TTCTCAACTT AGAAGTCTGC CTGCTCTAGA TTTATTGCAT TTCAAGTGCC 480
GCTTGAGGCT TCCTTGGCAG GGCAGACCAA ATGACCTTGG TGTTTTATAC GGCCCGTGGG 540
CCAGAGGTTC TCATCTCTGC ACTAAAGGGT TTGAGCAAGG AAGAAA 586

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

TGGGTTTATA ATTCTAAGCA AGCACAACAG TAAATCATTT CTATATCTAA ACTGTAGCAC 60
TTTGAAATTC ACGAGTAGTT TTGCCCATTT GGTATGTTTT TTATACTGTG GTTTTAAAA 120
AGTCACATCT GGTGCCATTT TATTGCTGTG AAAGAATCGC GTCTTCATTC TAAATCTAAG 180
ATAATATTCT AATACTTTTC CTCAAAGAG TTCTTAAAAA TTTCTAGAAT GATCTTGTC 240
TAGTTTCCCA TTTACTGACT CTGTAATGAA TAAATATTTG AAGCCATAGC AATAATTTTT 300
CATGCATATG ATACTGTCTT AATAATTCCG TTGTGGCTAT GCGCTTTATT GATTTCTGTG 360
CCACTTCTGT GGCCTGAAGT GAAATGTATT GCCCCACGGA AGCCATTATG GTTTCCTTTC 420
GAATTACGGC TTTACTGGCT CGCTCCTGTG CGCGGGCTTC TTCTCTGTCT GCAGTGCCTG 480
TTGGTCCCT GGGAnTTACT GGGGnCTGG ATTCCCCCA TCGCCCTCGC CTTGTCCTGT 540
GnGTGGAAGA TGAnGACAGG AAAGTTGGGA AGAAAAATGC AGCAGGCAGC CAACCCTGGA 600
GAAACCGCTC TTCAGACTTC CGGGnChCCT GGGCGATGGG GCATCCTTCC TGCAAC 656

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

TAGGTTGTGT nCCAGAATTG CAATCTTCAT CATGTACTGG GGCTTAGAGC TGCTCTGTTT	60
CACACCTTCT CCCCCCAGA AAAAAATCCC CACTGGACAC AACAGACATG CCTGAGAATT	120
TAACCACCTT GCATATATAG CAAATTCATT CACTTATTAA TACCCACGTA ATTTAATATT	180
ACTAAACATC AAGCAAGTAT GTATTAGCAT CAACTTCTTG CTAGACAGAC ACTATTTTAG	240
AAGTTGAGAT TCAACAGTAA CTAGAGCAGA TACCAATACC TGCTCCCAGG GGTCTTACAT	300
TCCATACAAA GAAGATAGAC CATCAAGGAG GAAGACAGAC ACTGGTAGGA GGAAGTCCT	360
TCACCCAAAG CTTTGTCTTCT TGGGGCCAnC TGGCTTCCAA AAnGAGTTTT AAGTGTGTCT	420
GGGCATAAGT CTGCCAAGTC CCCAGCTCCA TGTGCCTTCC TAAGCCCCGA GGTTAGTAGT	480
GGAACCAAAA CATCTCCACT AGAACAGGGC AACCGACAAG ATTTCTAAC ATGAAAGGGC	540
TCGGTATGTA AGAAATGAAG TAAGTGAGTA GTTTGGTGGA TTAT	584

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

AGAATGAGTT CTCTGTGTGG AGATTACACC AGCATCTGCG TCCATTAATG CAAACGTCAC	60
TTACAAGCAG GAGTATCTGG AAGGAGGATT CTTGAGCTGA AGTCCAATAA GAACAGTTAA	120
TCCACATTTT GAGCTCTCTT CCGAAGTCTG AGGCCAGAGG GAATGAATCC GCCAAGATGT	180
TTTTGATAGA AAATAACAGA AAATCCAACCT CGAACTGACG CAAACAATAA GGAGATTTTA	240
TTGACTCACT TAACTGGAAA GTCCAAAGGA ATTAAGCTTC AGGTGAGGGT TGATCCAGTA	300
ACTTAATGAT TTTGTTCTCG GTATGGGATC CTGTGTTACT TGCCTATCAC TGTGTAGCAA	360
ATCACTGGAA ACTTAGTGGC TTATAGCAAC AAAGCCTTTT GCTTATCTTA CAGCCACGGT	420
GGGATAGGAT TGAAGAGAGG CTCAGCTTCT GCTCTGGCTC AGACTCTCTT ATGAGGGTAC	480
AACAACAAAG GTGCCTTTTG GTGGTGTGAT CATCTGAGAT CCTGAGGACT GGAAGGATGT	540
GTTTCTGAAA TGGTCCATTC ACACAGC	567

948

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

TTATATATAT GGCTGTGCAA GTCCCTTCAT CCCTTGACAT GAAAGCAAGA AGGGAAGAAT	60
GTAGCCATGA TCATTGGGAT CAAGGTCAGG CCATGCTACT CACTTGCTGC ACATCTTGGG	120
AAATTACTTA ACTCCCTGAG CATCATGTCC TPTCCCTGTG TATTGCCGCC ACCTCATCTA	180
GCAATCCCAC TGCCAGGTAT GCGGCCAAAA GACACTAAAT CATGTATCA AAGAGATACC	240
TGCCCCACCA TGTTTGTGTC AACGTTGTCC CCAATAGCCA AGATATGGAA TCAACCAAGA	300
TGCCCATTGT AAGATGAATA AAGAAA	326

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

AGTGGAGCAG CCAGGACACA AACTGGCACC CCCGTGGGAT GCTGGCGCCC CAGCGCTnTT	60
CCCGGCTGTT GCTTCTTTA ACTGAAGAGT AGGAACTGCA CACGTGTGTT GGGTACATGT	120
GCACATCGTG TCTTGCGGTT ATTCGTGGAG GTCAGGGTCT GAAGTCCTGG CAGACAGCCT	180
GGAGGGCGTG TCCAGCTGG TGTGTGACAG GCCCCCAGGC GGATAGCAGT CTCTGTCCTC	240
ACCGCTCAGC AAGACGCCTG GCAGGGAGGG GCGGGCTGCC GCCCTCCTTG CTGGCTGGGC	300
AGGTGGGGTG AGGTGCTCT GCGTGCCCGC CCGTCTCACC CCTGCGTTTG CCCCATGCAG	360
CGGACCGGCC CCGTCATCCT CGGCGCCAG CAGTGGGAGC TCAGACGACG CCATCCGCTC	420
CATCCTGCAG CAAGCCCGCC GGGAGATGGA GGCCAGCAG GCCGCCCTGG AGCCCCCGT	480
GAAGCCCACC CCGCTGCCGC AGCCCGACCT CGCCCTGCTC ACCCCCAAGC TGCTGTCTGC	540
CTCGCCCATG GCGGCCGCGT CCAGCTACGC TCCTCTCGCC ATCTCCCTAA AGAAGCCTCC	600
GGnGGCCCCC GAGGCGGCGC TCGGCTC	627

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

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AGATTTGAAG AnACACTACA GAGAAATTAT CATCAAAAGA GCCTGGTACC GGTACAAAAA      60
CAGACAGATT AATGGAACAG CATAGAAACn CCAGAAATCC ATCCAAGCAT CTACAACCAA      120
CTTATCTTTG AAAAACAGTT AAAAACAGnC TCTTCAACAA ATGTTGCTGG GAAAACTGGA      180
TAGCCACATC TAGAAATATG AAGCAAGACT CCTCCACCTT AAACAAAAAA TCCTCATTA      240
ATGGATTAAA AACCTAAATT TgNACCAAA TGCAATCAAA TTATTAGGGA AAATGGGAGA      300
AACCnGCAA GACATTGGTA TAGAAAAAAA TTCTTAGAAA AGACTCCAGA GGCACAATCA      360
CAGCCAAAAC TGGCAAATGA GATnACATCA AATTGAGAAG AT                          402

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(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

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ACCCnTTTTT CATTTCTGGG AAAAACTTAA GCCTGTAACA TTGAAGAACC CAGAGGAAGC      60
CAGTGAGATA GCACTAGTGA GAGTTGGGAT GGGATGGAAG GTTAGCTGAA ACCTGGGGAC      120
GGAGGCGGCA CCCCTGTGGT TGGCCTGAGC GGGAAAGGTAT GGAGGACGTG GGGGGACGGA      180
AGTCGTCACA GGGAGTAGGC GGGGCTGTGC GTTCTGTGT GCATCAGCGG TTGTTTTGCT      240
GTGTGGAATG GGGATAGGGC ATATATTTTC CAGATTTTGC TTTTGGACTT TGAGCTGTCT      300
GTTTCCATCA TGGGCATCGG GCCCGCAGTT AAAGAGCGCC AGACTCCGGC GGATGGGAAT      360
GGACCGTGCA CCCAGCAAG TCTGGCTGAG TTCACCTGGA GACCTTAGTA GCGGGGGCTG      420
CCTTTTCCAT GGCATTGGT AGTTCCAAGT TTGACTAGTT AACCATTAAT TTTTATGGAG      480
CTTGTTTCATG GGAAAGAATT TCATGTTGCT ATGGGAATGA CCATTGAATG CCGGCCCTGG      540
AAAACAGCTC AGGGGCCTTC TATCACCAGT CTATCATCTG TTAAGTGTGA CAGACACTGG      600

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950

GGATCAAAGA AGTTATGGCA CCTACCCG

628

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

CATTAATCAT CCCACACTTC TGGGTTACAC CAACAGGCTC CCGTTGCACC ATCAACAAGA	60
AAGCTATAAG GCAATCATCT CCAGTAGTAA CATTAATTCT AGGAAGCTTA CTCTGCTGAA	120
ATAACAAGT GAGTCAGAGG TGGGATGGGG AGAACCGCAC GGACCCAAGA CAGGAATCCA	180
CGTGGTCATG GCTGTGCTGT TGATCCAGCT GAGAAGTCAC GTGGACAGGG ACTGTGGCTG	240
TGACTATGGG TCTGACGAAG CAGCGGGACA GGAGGCAGGG GCTCTGAGCA TCCGTGTCCC	300
ACCCCAACTC ACATTCTACC CGACACTG	328

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

AAGAGTTCTT CCTCCCTTTG AGAAAGAACA AACTGGGTC CCCCACAGG AATGGACACA	60
TAACAGCAAG GCCTGAGTGC TGGTCAGGAG ACATGGACCC AGGGAAAAGT TCCAACCGTG	120
GAACCCTGGC CTGGGAGGCA GAGGCCAGCG GAAGGTTGGT TCTTTAAAGA CTCTGATAGT	180
ATGCACGCAA GATCATGTAC ACTGTGACTT AAATTCAAGG TTACCTTCTA TTGAGTCTGC	240
ACGCTAAAAA CAACAACAAT AATAATAAAT GCAAAGTAT TTGATGATAG CCTCGGAAAC	300
CCAGCGAGTG AAAAAACCTA CTGGCAAACA CAGACTCTAA AACAAGCAAA AGCAACTGCC	360
AAGAGCCAGC TGCCCCAGCT TCAGGTGTGG CTGAGCCACA CATGGCTGTA AGCCACAGCA	420
CCGCCAGCCA GCCACAGGCC ATGAGTATCT GCCGCCGnCT TCTCCCTCTG CCCCTCTCCG	480
CTTCCGT	487

(2) INFORMATION FOR SEQ ID NO: 381:

951

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GTGAAGTCAT GGACCCAGT AGGCCTATTC CCCTGTGGAT GAGTGTCTTC TGTGGGGGTC	60
TTCAATGTTT TGGCACTCTG TGCACGTGG TCGGTCCATG ATGGCAGGGA ATCGGCTCGC	120
TTTTCTTCAC AGCCCCCTAA GCACCTACCG CAGGGTGGGA ACTTCCAGCC AGCCCAGGCC	180
ACATTCGGCC AGCAAAAGCA TTTGGTTTGG CTCTGCCAAG GGCAGCCACA GGCGGGGACT	240
CAAAAGTCAG TAACTCTCTA GCAAGCTAAT TTTTAAGTTG ATAATTTTGT ATGGCCCACA	300
AATGATGTTA TAAATATCCC AATGGCCCTC GGCAGAAAAA AAAAAGATTT CCCACCCCT	360
GCATAGCTGA AGTCCTAAGT TGTACTTGGC CAAATGCGCT CTGCCTGCCC AGGAAGGAGT	420
CCTTGATGT CCTGTATGTC GCTGGCATGG GCACTGAGGG AGCAGCAGC	469

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

TTTTAAATG CTTTGTGGAA GTCACAATCT AGTTGGGGAA GTGTCGAGTT CATGCCTTTC	60
CTTTTAAAAA GATTTAAAAA GAAGAAATTC AAATCCATC ATTTGAAAAA GAAAATATTT	120
AAAAAGAGAT TTAAAAAGAT GTTAAAAGAG GGAAGATTTT TCCCTTACCT CTCCTTCCTT	180
TTAATATAAT ATCCAAAATA TTAAAATATA TTATGATATA AGCATTTATA TTATTGTCTT	240
CATATCTAAT TTTTCTCTC TTTAACGTTG TTTCTTCAG TAACTCAGAC CTTTCTGAG	300
TTTAAATTTT CAATAATAAG AAATGAAGGA ACTTGTCAGA TGTGCTAGT CAGGAAGGCT	360
GCCATCAGGA CTCTGCTGGA AACTACCTTT CCCCATGCAA ATGATTGAG ATATTGATAG	420
CATTAATTTT TTTTCAAGG TACnTATATA GAATCCCATT ATTCAAAAGG	470

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs

952

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

ATACCACGTG GATCCAGCAA AGTGCTTCTG CAGAGCCAGT CTGACCTGGG GCTGGCCGGC	60
TGCTTCCTCT GGCTGGGCAT GGCCAGACCC GCTCCTGGAA AACCCCGAGA CATCAGAGGG	120
AGCCTGGGGG GCCCCGCAGA GGGAGGCGGC CCAGCGCTGA CTCCAGGGAG ACCCCCCAC	180
ACCCCCACAG CGGGCTCAGG GCAGGGGCCT CGCTGAGGAG CCCAAGTGCT GCCCTCTAGG	240
GGTGACCCTG CAGCTTCCGG GGCCAACCTG ACTGCAAACA GAAGCAGCAA AGTGCACAGT	300
CCCTGAnCCC CCAGACTTCG AGACAACACC CGCTGTGCCC CTGCCAAGAT GAGGGTGCGC	360
CGGCATGGCT GAGATGCGTG GGGGCGGCTC TCCACCCCTG TTCATCTCTC TCCTCTTCAT	420
TGCAAATCCT GCTTCAAGAG CAGACCAGAG GGCAGGCATT TGGCACAGAG TTAAACTCTG	480
AG	482

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

GGACCGACAG TGCGCACGGA GGCCAGGTCA CCCCTCTCTG TGTTTTCCAG ACACTTACAA	60
GACCTCGGA ACAACCCTGA CAGCAAAGGC GCTGCAGGAG CTCTTTCGCA GATGAGAAGC	120
CTGAGTCGGG CAGAGCTAGT AAAGGCCAGG AATTGGCCCC AGGCCCTTG GAGCCAGAGG	180
GCCTAGCATT TCCCTTCCTC AAGCCATCCT AGAATGCTCG GAAGCAGAAC CCGACCGCAA	240
GCTGATAAGG GAACCTGTCA CGCATAGCGG GAGCGTCCCG GAGATCTGAG CTGTGGTCCT	300
CAGGGGATGG GCCTGCGTCA TCGGCCACCA CTGCCGTCAG CATGCCGCCC GGTGTGAGGA	360
GCGAAGGCTG TGACGGGAAG GACTAACGGG AGTGAAGGAT TACTCAGATT GGAntGTCCC	420
TGTTCCGGGG TTAGTCCAGG ATCAAAGGAC GGGCAAAAAT GGGACC	466

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs

953

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

TGAATTCCTA AAAACAGGAT GTTAGGATGC CTTGGT'TTTT CTAAACAGAC AGAACACTGT	60
TCCCCTGTTT TAAGTATATT TGGGAAGGGG TGAAGGGAGG TGGAAGGGGA GAGGCAGTCT	120
AGTATACTTA TTTCAAGAGC AAACACAGTC TGATGAATGC CTTGGATTGT TCTTGATGCC	180
AGCTGACTTT TCAGCACTCA TTAATGGCTT CCGTGTGTGC ACAGTCTTCC AAAGGCATGG	240
AGAGAAACCA TCATGCACTT AACCTCCATG GCATTGCTGT GTGGTATCCG GGCCCAATGT	300
CCCCACCCCA TTCCAGTGTG TCCTCATTTG TAAGTGTGGG AAAGAGCACA GAGAAACCAT	360
CATATCAAAT CAGAGCTGGT GTTTATCGAA CCCCCATAAT GTCAGGCAGT AGACA	415

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

GGCACACCTT TTAAAATGTG ACAAGCGCTC ACACAGCAGC TTGCGGGTGC CAGGCCAGCT	60
CTAAGCTCAG GAGCATCACC ACGGTAACGA TGGTACCCAC ACCACATCAC CAGCACACCA	120
CGGCCGCCGC ACACAGTGGG CACCCGGGCC AGCGGCACGC CTTACCATTG CTCATGCACC	180
CGCATTTACT CGCAGCAACG GCCTAGCGAG CGGGGGTCTA TTCTTAGCCT CACTCTGCAG	240
GCGAGGAAAC AAGGCCAAGC CCTTGGAAGC TTGTCTTGA GGAGAGCCAC GCGGGAAGTC	300
CTGCAGCCTC TGGCCACTGG GACGCAGCTG CCCGGGGCGG CAGACACCCT GGGAGGGAGC	360
TGCATCCTGC CGGCCCTCCC CTTCCTGAGG CAGGCCTGCA nTTCCTGTTC CGCCTG	416

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

AAAAGCACAG ATACTTTTTC CTGAGCTGAG AGCACTGTGA AGTCCCACAT CCATAACGGG	60
CAACCCTTCC TGTGAGAACC CTTCTGTGGA GCTCTGAAAA GAGAACTGTC AAGGGCAAGG	120
AGGCTTGTTT GGTGAACCAG GAGTCCTAAG CTTTGCTCTT TGCTCTGTCT AGCAAGTTT	180
CAGTTACCTG CAGCCATTTC TGGGTTAGGC TCTTTTCAAT AGTCACTTCC ATGGTTTAAG	240
TAGGACATAG TTCCTGAACT CAAGCAGACA CTTAAAGTTT AAACCCAGG GTCTTATGGT	300
ACTAGTGCAG AGAGAGTGAA AAATGGGCCT CATAGACGAT CCTTAGTTCA CTGAGACACA	360
CCCTTAGAnG GTAGCTCTCA TGAGTTGAGT TGGGTCGAAC TCTTGCTTCT GGGCTGCCAT	420
GTGACTATCC TCTGTCATGT CATnCTGGT CTCACCAGAC AGGCAAACCA AGGGGCCTGA	480
CCAGTTTGA GGGTCTACTC CAAATAAACA AACCTCC	517

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

TTCTTTTGTT ACCTGTGACA TGGATACAGT GCTTTGCAAA CTGGATAACT GAGGCCATGG	60
CCTCTGAGAG GACAGAAACA GGCCCCACCA GCTCAGGGCC CTGCCAACCT GACTCTTCAT	120
CTGGTGACTT GATGATGCAT CCATCTCAGG CTCCAATCCA ATGAGAAGCA CTAGTGTCCA	180
GATCCTAACC ACAAGACTAC TGCTGTCCTT TTATGGGCTT CCCAAACCTG TGTGCTTGTC	240
CAGAGCAGCC CACCCAGCTG CTTTGTGACC TTCCTGGAGT GGCGGCACCA CCATTTTGAG	300
TGCACCGTGT GCGAAAACAA AAACAACAAC AAAAAGCAGA AGGC	344

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

TTGGCTTTCT CCTTCCGCCT GCCTGGAATG TGGCTGTGGT GCCTGACCCG GCTGCAGCAG	60
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955

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TTTTGCAACC GGATGGAGGG TAAGGAGCCC AGAGCAGATG TTAGAAGGAG CCTGGCTTCC      120
CGGTACTGGG TCCCAGCTAC CACATCGGCC CTGGGCTGCC TGTTCCTTTT TGTTTGTTTG      180
TTTAAAAATT TATTTATTTG GAAGGCAGAG TTAGGGAGAC AGAGATCTGC CATTTGCTGT      240
TTCGGTCCCC AAATGGCCAT TAACAGCCGC GGCTGGGTCA GCCCGAAGTC AGGGGCCTGG      300
GGCCCAAGGA CTTGGGCCAT CTTCTGTTGA TTTCCCAGGC ACATCACTGG GGAGCTGGAT      360
GGAAGTGGAG CGCTGGGACT CGAACCACG CCGCCATCGC ATGGTGGCAT AACCCGCTGT      420
GCCACAGCGC CAGCCTTCCC GCACCGCCTG TTGGTCCAGG TCCTGGCTGC CAGGAGGGAG      480
GCGGTTC                                           487

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(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

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AGGAAACAGG AGACAGGGTG CCTGGGCTTT GGGCCTGCCC ACTGCTCCAC GACACGGGGC      60
AGCTCACCCC CTGGTCCAGC CTGGTTTCGG GAGCGGTGCC TGGAGCAGAG TGCCCGGGGA      120
GAGGCCTGAG CTGAGGAGGC GGACAGGGCC AGGACGCGGA GGGCCTCCCT TTGTTCCATC      180
GCCTGCCAAG CAGGAAGGCT CTCCCAGGT GATGCGCCTT CTCTGGGGCC GCTTCCCTCC      240
TGGGATTCGT CACAGCAACC TGAGTCTCAG GGAGTGTGCG TTAATTATCA AACGCTTCAC      300
AAGCATCAGG AGCCCGCAAG GTGCTTCACC ACCATAAAGC ATTTCTCTC ATTAGTGTTT      360
ATGATCATAA AGCTTCAGAT GCGGCTCCCA TGGCAACCTT AACTCCTCTC CTCCCCCTC      420
ACACACACAC ACACACACAC ACACACACAC ACACACAAAC ACACAGTGAC AGGATTTTTT      480
ATTGCAGTAA TAACTGCAGC TCGTAAACCT GCCAAATTAT GGGGAAACAT TTATTTTTAT      540
AAGCTGAGAT AAGTAGGCAG CGCGGGGTA GCAGATCCTC GCCTTGGTGG CTCCAGAACA      600
AGCTGGTCCT CAGACTAAAG ACATTCGCAA G                                           631

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(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

CATTTCATA TATGCTAAAG CGATTGTGT TGTGCTAACC ATGAGACTTG TATAACAGTC	60
ATAGTATACT ATTTTtagta CTTCTGTAG CTTTAGTTAA TTGTGATCAT TCTGATATTT	120
AACTTTTCAT GCTGGGGATA CATCTAGGTA TTTCCTTTTG GTATTTCCAG CGCATTTTTC	180
TCACCCTCAA TCATTAGGAA GGATCCGGAC TTACAAGATA AAGCAGTGAG CAGCACTCAG	240
AAGCCATGTG CTATTAATTA GAGTGGCTCC ACAGCGATGG AACCCATCCC ATTGCAGGCT	300
GGCTTGCCAC GGCCATTCTC CTTCTTCGAC CTCTGTGCCA CCAACTATCC TGACACTCTG	360
ACCTGCGGAT TTA CTCTTC GTGTCCCACA ACCTGTCAA GAGATAGGGA TGCAGTAATT	420
AGCAATGTTT TATGTATCAA TGGTGCTACT ACATCCCAA TTCTTGTA CT TGAGCTCCAG	480
CAATATGAAG TACTTTTTTC AGTGTTCCTA CACAGTAGAT TTATTTTCATT AGCTACTCTA	540
A	541

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

ATTTTAAGGA AGAATCAAAA TGAAATGAAG AAAGTAGTAG AACAGGAAAA TGTGATAGTG	60
AAGAGAAATC AAAATGAAAT GAAGAGCTCA ATAGATCAAA TGACAAATAC ATTAGAGAGC	120
CTTAAAAACA GAATGGGTGA AGCAGAAGAG AGAATATCGG GACTTAGAAG ACAGAGCACA	180
GGGAAACAT ACAGTCAAAC CAAAGAAAGG GAAGAGGAAA TTAGAAATCT AAACATATTG	240
TTGGGGAATC TACAGGGATA CTATTTAAAA AACCAACATT CGAGTTCTAG GGAGTTCTTG	300
AAGGCATGGG AGAGAGAGAA AGGCTTAGAA GGCCTTTTAA ATGAGATACT AGCAGAGAAC	360
TTTCCAGGTT TGGGAGAAGG ACAGAGACAT CCTACTACAG GGAAGCTCAT AGAACCCCA	420
GTAAACCTGG ACCCAAAAGA GATCCTCACC ACGGACACGT GGTAATTTAA ACTTACCACA	480
GTGGAACanT AAAGGAAAAG ATCCTAAAAT GTGCCAGAGA GGAAAnGGCC	530

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs

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- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```
ATTCAATCCT GTTAnTTTCT TCTCTGATTT TCATnTTTC TCTTCTCCTA CTAGATTGCG      60
GATTGGTTTG CTGCAGTTTT TCTAGGTCCT TGAGATGTGC TGAAAGTCAT TTATTGGTA      120
CCTTTCCAAT TTCTTGATAT ATGnCCTAT TGCTATAAAC TTGCCTCTCA GTACTGCTTT      180
TGCTGTATCC CATAAGTTTT GATATGTT      208
```

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

```
GCCAATCCCA CCGCCCAAAG CCGAATATAA CTCATGACAT CTGCAAATAC ATTTACAATG      60
CCCAGCAACG CATTAAATTAC GTTTTTCATA CTGTCTGCAA CACTCTGCCG CACACTCACC      120
CGATAATTCA CAAAGATAAA ATTCAGCACA AAACCCGCTA TTATAGACCC GACAATCATG      180
CCGGCAAGC      189
```

(2) INFORMATION FOR SEQ ID NO: 395:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 585 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

```
CTCACCCATT TGTGCAGATG CTCCTCAGTG CTCTACTCTT CACCACCTGA GTTCACTGCA      60
TTCCCTAGGA AAAACTCAAA ATGCAAATAT TAGCCTCTCC TTGTAGTAAA ATGATTGCAT      120
CTCATGTCTT GTGTGAGGTG TGAGGACCAG GCCATGTCCT AGGGGTTTTT CATCCCTGCA      180
GCCAAGTGCC TTGGGTATGT TCAGTTTGCA TTCCCCTAAA AAGTAGTTCA GAAAGTATGT      240
TTCTCCCCAA AATAAAGTCA TAACTGATGT TGATTTATAA AGATTTACTT ATTTATTTTG      300
```

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TTTGTTTCTT TTTTTTTATT TGAAAGACAA ACTGGCTGCA GCAGTCAGAG CTGGGCCAGG	360
ATAAGCCAG GATCCAAGAA CTCCATCTGG ATATCCCATG CAGCTGACAG AACTCAAAT	420
ACTTGACTCA TTATCCACTG CTTACTAGGC ATGTTAGCAA AGTGTAGAT TGAATGCGGA	480
GTAAGCAGGG ACTCAAACCA GCACTCATAT ATGGGTACAG GGGCCCCAGA GTGTCAGCTT	540
AACCCATTGn ACnATACTCA CCCCCCTATG GGGACTCTAA AACAT	585

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

GTAGCAAAAA TATACCATCT GCAGTTCCAA TTATCTTGCT AGAATTATAT GTTTGACAAA	60
CAATACATTA ATTATAACCA TTTTATCAA TTTTACAAGT GTCACTAAAC CAGTTATTTG	120
TATCACTTTG TTCCGTGATG AATTATGGAA AGTAAGCCCT TTAATTTTGA AGCATTTTAT	180
CAAAGTACAA TATACATCCC AAGAAATGCA CGTGAGGTAC AAATGAATGA GGTTTTTGCC	240
ATCTGATCAC ACTCATATCC AGCACTCAAA CTAAGAAAGG GTTAATGATA CCTCGAGAGT	300
TCTAACTATT CTCCACATTT CTATTGTTTT GAACATGTGA AAGTGTATCA TCATGTATGT	360
GGTATGATTC AGTGAAACAC AATTTATAAC TATATTTCAA ATTATACGAC ATCCACATAG	420
TATTTATACT CTCTATATTC ACTATTAAAA ACAAGAATGC ATGTGGTATT TTTCTTTTAG	480
GGTAAGACTT ATTTCACTTA GAATAATGGT CTCCAGTTGC ATCCATTTCA CTTTAAATGT	540
CAGGATTTCA TTCTTTTACA GCTGAGTAGC ATTCCATCAT G	581

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

GTCAGAAAAA TAATCAAAGG CATACAAATT GGAAAAAAG ATGACAAAAA TATTCCTATT	60
TTAAGATAAC ATAATTCTTT ATTTGAGGAA TCAAAAACCTC CACTATTAGA ATTCATAAAC	120

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AAAATTTGAT AAAATTTTAG GATACAAAAT CAACTTACAA AAATCAGTAA CATTCCTTATA 180
CACTTACAGT GCTCTGGTTG ACAAAGAAGT TACAAGTTCA GTCTCATTCA CAGTCATTAC 240
AAAGCAATTA AATACCTTGG GATCAATTTA GCAAAGGATG TGAAAGCTCT CCACAACCTGA 300
AATTACAAAA TGTTAATGAA AATTATAAAA GAGACACAAC AAAATAGAAA CATTTTCCAT 360
GATCATGGAT TGTAAGAATC AGCTTTATCA AAATGTCCAT ACTACCCAAA GCAATTTGCA 420
GATTCAATGT GGTTCCAATC AAAACACAAA GGnAATTCTT CAAATATCTA GAAAAAATA 480
CTAATGTTCA TATGGnAACA GAAAACACCC TGGnAAACAA AAGCAATTCT AAAAAATTTA 540
AACAAAGCCA AAGGGTCACA ATACCAAATT TTAAAGCATA CTATAGGGGC TGTTATAATC 600
CAAACAGTCT GGnTCTG 617

(2) INFORMATION FOR SEQ ID NO: 398:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

TGCTTTACTG CTACCAGACA GTGGGGTGTT TTCCTTCTG CTGCACAGAA TTTTACAGG 60
GATTTAGCAT TTCCTAAACG GTATTTTCATA AAGCCTTAAC CGATTTCCTCA CAAAATAGAA 120
CTGGGTCCTA GATTTTCACC TTCATTTAGA AATCCAGTCT ATCAGGATCA ATTTTACCAC 180
TTTTTAAATC ATTTTAGAAA GATACACACT TGCCTCCCAG TCATCGTGCT ATAGGAAAGA 240
TGACACTGGG GCTGATTTTG ATGTCTCCCT GAGTGGCTTT TCTTCTCATG ACCTTAAAGC 300
TGCTAACAGC AGTCAATAAT TGAGGAGAGG TAGGCGGCAT TATTTTTTCT ATTTAAGGGT 360
CAAAATTTAA GCTACTTATA CACTGCCATT TGTGCTCTAT CTCTGAACTG ATAACCTACT 420
CTAGTGTTAC AGCAGTCTAC CCAAAGAGGG AATCCAGGGG CCTCAATTTT CTCTTGACAC 480
TACACG 486

(2) INFORMATION FOR SEQ ID NO: 399:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 666 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

ACAGGCCCTA TCCTATGGCT TTTCTTCTG CATCTCTTCT AAGACAGGCT AACGGGGACA	60
CAGATGCCTC CTGGGCAGCC AATCCAATCA GGAAACCAAT CCAGAAGTTA ATGTGAAGGA	120
CAGTGAACC TCAGGCATTG GTTCAGGAGT TACGGAATTT GTGATAGTTT TAGAACCTGG	180
GAAATAATTT TCTATGTGGT CTCAAGAAAA CTCACTTTCT ATTTACAGAT AATTCTCCTC	240
CTCCTCCTCC CCCTTCTCCT CTCCTTCTT CTCTTTCTC TTATTAAAA AAATAACATT	300
TATTTCAAAG GAAGAGTTAC AGAGAGGGAG ACAGAGACAG AGTCTCTGCA GTAGCTGGGG	360
ATGGTCCAGG CGAACAGnGA GCCTGGAAct CTATTTGAGT CTCCTACGTG GGAGCAGGGC	420
CCAAGTACTG GGGCCATCCT CCCCTGCTTT CCCGGCACAT TAGCCAGTAA CTGCACTGGA	480
AGTGCGCAGC TGGGTCTCCA ACTACACTCA TACTGGATGC CGGCATTGCA AGTGACAGCT	540
TAGGCTGCTG CACCACAGGT GGTTCCTCAA TTTTCATTTT AATATATGTT CTGAAATTTT	600
AACACATAAT TGTACTTGTT TATAGGATAC ACTACAGTAT TTTAATACAT GTATTCACGT	660
GTAATG	666

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

AGTTCTTCCC GAGACACAAT TCCTCATGCT GGCCGTTTTG TCTTGCCTTT CTTACCTTCC	60
TCCTCTAGGA ATGAGGAGAA AAGAGGGCAC TGAGAGAGAG GGTGAGAATA ATCGCTCTTT	120
TCCTCCCCC CTCTGAGCGT GTGCTCTCTC TGAGGCTCAT TTCATGGGGT TGGGAGTATG	180
GGGAGAAGGG GTGGCAGGAA CAGAGGGTCC CGTGTGATCA CAAGAGCATG CACTGTTTCC	240
ACAATTATTC TAAGTTCAGT AACTACACAG CGTGGCTATA TGTTTCATTT TGCCTGTCTC	300
TGAGTGCTTA GAGAGCTGGC CACACGTTAT TCTGGGTATG TCTGTGACGA TGTCTCTGGA	360
TGCCATTACC ACACAGAAGG TAAACTGTAA ATGCATGCCC TCCCCAGAGT GGTGGGCTCC	420
GGCAATCTGC TGAAGGCCTG AACAGAACAA ACAGCAGAGT GAGGCGATCT ACTGCCTCTG	480
CCCGG	485

(2) INFORMATION FOR SEQ ID NO: 401:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 563 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

GACATTTCTA AAAC TAGCAT CTGAATTATG GGAAAAGACT TTTTCTCAC CTTAGCTAGA	60
TTAATGCAGA CAGAAAATCG GTTTAATATT TGTGTGGACT AGGGGTGGTG TCTGTGTGGT	120
GTTTAAGTGA GGCATGTGTC CCATATTGGA GAGGCTTTTT CAACTACAGG CTACTCTGTC	180
TCCAATCCAT TTTCTGCTA AAGTGAAC TAAGGAGGAGG CAGATGATGG CTCAAGTATG	240
TGGATCTCTG TCACCCATGT GGGAGACCTG TAATGAGTTC TGGGATCCTG TCTTCAGCAT	300
AATATAATCT TGACTGTTGG GGCATTTAG GGAATAAGCC AGCAGATAGA GATCTGTTAT	360
CTATCTATCT ATCTATTTGT GTTCTGTAA TTCAAATAAA AATGGAAATA AAATCAAAAT	420
GAAGATAAAC ATTTGTGTTT ATAATAGTTT ATTCAAGATG ATTAAATTCT AGTGTAAGG	480
ACCACTATCA CTTGCAAAAC ATGAGAACAC TGTGGATGGT AAAATCCTCT TGCTATTCTT	540
ATGTGAAGAG TTAGACTGCA CTT	563

(2) INFORMATION FOR SEQ ID NO: 402:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

CATCACTTTA AGTTGAAGGT ACAACCTCAT GTGAACTCA TGAATCTTT GAAAATGTAA	60
TGTGGCTCAC ATGGAATGTT CAGCGTGCCA TGCTGCCCTC TTACACTTGG AACAAAATGA	120
AGAGAGATGA CCAATTCTCA TGTGACAGTG ATGGAGCCCA ATTATGGATG ACTACCATGA	180
TATTCTTTTG AAGAGTCACT TGAGCTAATG AATTAATATA TTAATTTATA TTGTTAATTT	240
TAACATCTA ACACAGTTAC TATTTATGTA TGTATGAACC ATAATATAAT AATTTAAGGn	300
ATTTCCACAA ACAATGTACT ATATTAGTAG AGAGTAACTA AACTTCTTCT TTGCnTTATA	360
TAATTATAAA GGATGTCAGA ATGATACATT TTCCAAACA ACATATACTA TAATATTAGG	420
ATAAAATAAT GGAGTTAA nT	440

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

ACCAnTGACG TTTTAGGnGA CACTTTATCA CCTTCTTACA CCCTAGATCA TCTACTTACC	60
TACTGTGGCT GCATGCCTAT GCCCTTACCA TGGCATTTTG ATCACCAGGT TAAAAACAGC	120
AGTTCTCAAA TTCCATGTCC CTCTACCATC AnnCATCACC TAGGAACTTG CTAGAAATGC	180
AAGATTTGGG ATCCACGTTG TGACACAGTG GGTAAACCA GATCTGCAAT GCCAATATCC	240
CATGTGAGCA CTCGTThAAA TCCTTGACTG CTCCACTTCT GATCCAnCTC CCTGCCAGTA	300

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

TTATAAATAA TAATAATAAA AAAGTGTGCA CAGCACAAAA GAGAGAAATG nTTCAGGGAT	60
TCAGAAGCTA GAAATTCACCT TCCAGGGThA nTGGGCCTTG GCCTCAGAGG TTTTGATTTG	120
GGTGTAAGTT GATGCTGChA GTCCTGAAAA ATTTGGGATG nnACTCCGCA nTGTGTATG	180
TATTGTAAGA ATATACACAA TCTTAAAAAA GAAAACAAAC AAACCAGAAA AACCCCTCTC	240
GnCTCAGTAA CTATATTTAC CCTGAGCCAA GTGCAATACC TGGCTCCAAG AAGATTTAAT	300
AAATCTTGTG TCTTAGCCAG ATCCCTTCAG TTAGCATAGC TATCTCTAGG ACAAAAATCT	360
GGTGAAAAAG AGAAAATGTA ACAAnTGACA AGTCAGTAAA ATCACACTTA GCCTGCCCAA	420
ACCCTTGACA GGCnTGTGA	439

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

AGGGCAATCA CTTAGATGCA ATGACAAGGn CAATATGAAC TCCAAGAAAA CAAAAATGTA	60
AAGTCTCTCT ACCATTCCCTA CATACTCAGC ACAAAGTATA TATTCAATGA CTAAGGCAAC	120
ATTTAAGAAT GAAGGCGTAG TAGTTAAAAA AAAATAAAAA CAAAGAATGT AACCATACTT	180
ACCAAAACCT AGGTTTAAAT ATAGTGGATT ATATACATTC AAATATAGAT AGGTATTTTT	240
TAATTACTGA AATCATTTTT AAAGAGAGTG GCAAAAGTAT ACCATTTAAC TTCTCTTAAG	300
AGCGGTATCC ACTGTGTTTA TCCTTATAAT TTAAAGTTAA AATTCTGAGA GGA CTCTGA	360
TnCAGAGGAG GCATCAGATA TCAAGTCAGG TTAACACAAA TGnCACTTT	409

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

AAATTGTTTT GTACCAAAAA TATTTTCATT TCATTTTCCA CATGACTTTT GAAGTACCTG	60
ACATACTACC CTGTACTCTT TCAGGACATT CTAGGCCTAA TAGGTTGCCC TTAATTCATT	120
TAAAGTATTT AATTAAATTA TTTCTCCCAT TTCACATATG AGAAACTGA GGCATGAATA	180
GAGACTCATC CAAGATCATC CACTAAGTCA CTCTATGTGG TGGAATGAGA AGGCCATGCA	240
CAGATGGCAC TGGCAAACAA GTGTCAGTTA CTCAGGAAAT GGCTTTGGAA CCCACCTGGC	300
AAAGGGGCCT GCCTGGCAAC AGCnTnGATT GGTTAGGGCA TAAACCTCCC CTTGACCAGA	360
TTGGCTGCCT GGCTATATAA GCTGCTGCAC CAACTGAAAT AAATGAGTCT GCAAGCTGCT	420
CACCTTTGGC CCGCTTTCAC CTGACTCCTG GTGTCTGTGT CATGACTCCA TGCCTCTTGC	480
CTGCACTGCA CTCCTCCTCT CAGAATGAGT CCACAACAAC ATCTCTAACA GTGTTACCCA	540
GAGTCCACCC CCTCTTCCAA GGCTTCAG	568

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

AGCTGTCTCC ATCCTACTTC AGGAGCAAAT GCTTTGTCCT CATGCAAAAA GCGCATACTA	60
TGATTTTACA CCTGGGATCT TCATCACGAT GTACGTGCAC AAATGTGCAC AGGACAACTT	120
TGTTTTTACA TTTTGACTCA CTTTCTAAAA ATGTAGGCTA ATAAAAATTG TTGATAACTA	180
CAAACTCTC CAATCACACA CACCCCAAAG CGCCTTCAAA TTTTCCAAAC TGTAATCTA	240
CAAGGTATCA ATATTACAAG AAGTACCTTC ATGGATGTCC ACTGAAATAA AGTCTCACTA	300
TTGTGCTTTC GGTCTCCAT TTTCCACATC TGTATAAAAA AAATCACACC TCGCTCTATA	360
ATTGAGTTTC AGAAATAAAG CTCTACTACA TGCATGTGCG TTCATACCAT TTCTATAAAA	420
ACCAAGGGCT CAGATGCCTT TGCACAGTGA AACAGATCAC AGTGAAACAG ATGATGGCAG	480
GCACATACTC TTCTCCTTGC TTCTCAGCTC CTCCTTGCTT GAGAGAAGGC AGGAAAGCAA	540
GCTGAGGGCA CTGCCATGTA TGAGGACCAA CCACTGTTTT AGTCCCTTTA CATGTGTTGT	600
TCTTATTTAA CACCTACAAC AGACCGAGGG AATCA	635

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

AACATCCGTA CCACTTGCCC TCAGGTAGAA GCTAACCACA AAAAGAAATG CAGCAACATG	60
AAAATGAAAT GAAATACCA AATAGACTGA GGCTTGCCTG AAACCTGTTT GTGCTACCCT	120
AAAAGGAGAC TAGAGAAGGC TAGAGAGCCT TGAAGAAAAA ATAAGAAGCA AAGACTTCAT	180
TTTGACCTA ATCGGAAGAC TGGAAAGACA ATTAAAAGAG GACTGCACTT CTGAGTGTTT	240
CAGTCGGACT TGCAGTCCCA TCCATGTTCT GTCTAAGATT GTCTTTGGAA GTGTGTTTGG	300
CCTAGTGGTT AAGATGCCTG AATTCCTGTG CAGAGCnCTG GGTCTCATG CTGGCTCTGG	360
TCTTGATTTT GGCTTCCTGC TAATACGCTT CAGGGGAGGC GGTGAGCAAT GGTCCAAGTA	420
CTTGGGGTCC TTTTACCTAT GGATTGAGTT CCTGATTCTT AAGTTCACTT CAGCCTGGCC	480
CAGCCCTGGC TATTGGATGT ATCTGGAGAG TGACCAAAGG GATTGTATCT TAGTTTGTCT	540
GTCTCTTTCA CAAAGATTAA ATTC	564

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(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

```
GGAATATTCT GATCATTTAG AACAAATTGA CTTGATAAAT TTCAATTGTA TTATTACCTT      60
CTAAATCAAA TAATAGTATA TATGTTTACA AAACAGTATT GATTTCCTTT AGTGAGTTCT      120
ACAAAATGCT AAATTTCCCTT TTAAATTAAA AATATTTGGT TGGTAGAGGA TGGCACTTGG      180
TCATGAAGCT AAGACACCAG TTGGAATGCC CACATGTCAT AGCCTGTGTT GGACTCCCTG      240
CCCTGCTCCT GATCCCAGCT TCCTGCCAGT GTGAATCCTG GGAGGCAGCA GGTGCTGGTT      300
CAAGTGGTTG GGCTTCTGCT GCCCACATGG GAGATCTGGA TGGAGTTCCC GCCTCCTGGC      360
TTCAGCCCTG GATATTGCAG GAATTGGAGA AGTGAAGCAA TGGACAGAAG ATAGCGCCTC      420
TCTTTCTCCA TCATTACGCC TTTCAAAGAA ATAAGATAAA CTTTTTTTTA AACTTTTATT      480
TAGTAAATAT AATTTTCCAA AGTACAGTTT ATGGATTACA ATGGCTnGnC CCCGCCATAA      540
TTTCCCCCCT ACCTnCACCC CTACCATCTC CCGCGCCCTC TCCCTCTCCC ATTCCATTCA      600
CATCAAGATT CATTCTCAAT TATCTTAATA TATACnA                                637
```

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

```
AGGACTTGAA GCTGATCTAG AAAGTGGGCT CTGCCTAGAC AGCAGTAGCA GCCCTGTAAC      60
AGGCGTCTGC CGGAAAAGCA CCAGGGCTTC TGCCCGGCTC CTCCTGAGGT GGGCTTTCCC      120
TACTTCTTCC TCTGCGGTTT TGTACTGCTT TCCCACGGTT TCCAAGCTGC CTTGGTTGGT      180
CGTTCCTTGT ATCTTTCTTG AAGGACCATC CTCAAATGCA GCTAGATCTC AAGTTAACAG      240
CCAGGCCAGG GTGGGTGGGG TGTCACATTC CTCCTCTGAG CACAGACCCC AGTCCCCCCC      300
TCAGTTCACA GTGCCGTTTG CCTCATCTGG GCTTTGCCAC TACTAGCTG TGGGACTTGC      360
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CATGAGTTGC TTAACCTTTC TGTGTTTCCC TCGTCTCAGC TATAAAAGGA AGCTAATAAC 420
CACCGCCACC TCCAGGATTC TGGGAGGCCT TAGTGAAAGC TAGGGAGAGC CGGGCGCTCC 480
GGCGGT 486

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

AGGATTGTTT TGCTTATGCA AGGAAGGCCT TTGAAGATGT TTGTCAAAC CTCTGTGATC 60
TGATGCTCTA AGTTGCTCTG ATGCGGACAT GTATTAGCAG CACATGTGTC TGCCTGTTGC 120
TGTTCTTAAT GTAGTCACCG ACAGCCTAAA TGCTTCTAAC GCCAGCTCAC GGGCACACTC 180
TTAATTGGTC ACTGTCCTTA AATACCCAGA GTTCCTACAA CCACGGCCAC ACCTCCTGGG 240
AACTAAGAGG GCTGTTGGCA ATGCACAGGA AGGAGGTCCA ACTGGGGCCG GGGCTCATGT 300
CCCCATCGAA GGAAGGACCC TGA CTGCGTT GCAACTGCAA AGCCTTTAAG AACTGTTTCT 360
TTTTATTATT TGTGCCTTTC TGGCCTCATT AATGAAAGAG CAGCTCAAGA TTCAGG 417

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

ATAGGCATGT ATACATATGC ATCACACACA TACAGATGCA TCGCAGGCAT CCATATAGAT 60
GCAAAGTATG TTTCTGCATG TGTATATATG AGTTTACACA TGTTTGTGAA TGTATTACCT 120
GGATTCTCT ATATAATCCA GGGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTTTTCATTT 180
CTCACCTGA ATCTGGAACA GTGTCTCCTT GGCTAAGAAA AAAAATCACA AGGCTCAGAA 240
GGAGCAGATA AGGGATTCTC CAGAAATCCC CATCCCTCAC CTGGGAGCAA CATTCCCTAT 300
TGACTTGAAA GGTAACAA TCAGTTTCCA CCTCATCTC CATCCTCTGT GTGTCTGAAT 360
CATATTTTTT CTCTGGGGAG AAGTGTTCCT GAGACTACAG AAAACTCCCT GGAGGACAGG 420

967

AAGACAGAGG AAAGACCTCT GTGGGTGAA GAGGCAATTG CAGGAAGCCC AAGTGGGAGA 480
G 481

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

TTATAAACTC TAAACATGTG CTCCCACAAG TACTGTTATT TCTCCAAGGC ATCACATTTTC 60
CTGGTGGTGG CTTCTGGTTT AACAGTCTGT GTCTTACACT CGAGCAGAAA CCCTGTGAAG 120
CCAAGGAGTT AAAATCTTTC ACCATCCCCT GCTATAGTAA AATATGGGCA TGTATATTGC 180
ACTTCACAAA TAATTGAGGG GGGGGGGAGT TGTTACACAT GAATGAGTAA CAATTCAGGT 240
GGTCCAACCTC TATAGTTAAT TTTTGATATA GTTAATTAAT TGATATAACT CCCTCAATTG 300
GAATGAAATC TTTCAGCAGA GAGATGATCA TCATCATCAA AATCTTCTCT GGGTCCCACA 360
TGCCTACACT CCATTGAGTT AAGAGAAAGA TACTATGGGG nGgNACCGTG GCTCA 415

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

TACTTTTATT CATTCATGAA ACGAGTCATT GAGCACACGG AGCACCGGGG TGAACACGTG 60
GATGTCACTG TGAAGGTGCT GGCATTTGTC CCGGGAAGTG CAGGCTTGTG AACGGATCCT 120
GGAAGGCAAG CGCTGCAGAG GTGCTGTGCG CAGACCACGA GCGGCTCTCG CAGCCATCTG 180
TCCCAGGAGT TGAACATCTG CCGCTTTCTT CTGCGAaTG TGGCGTTTCC AAGGGTTTTTC 240
TTCAAGAGTG GATGTTGAGT TAATGATTGT TGAGATTAAT TACTTCATCA GAATTCCTTA 300
AGAAAATGAC ATTCTATTA ATGTTTCCCT TCATGCCCAA ACCACAACTT TTACTCTTCT 360
TGATTTAACC TGCCTGGTGG CCTGTGAGTT AGGAGTTAGA TCCCCTTCAA ATTCTGCTC 420
ACGTATTCCC GAAAGCTCAC GCTCCCAGTT TTATCTCGCC GCCTCCCGCT GAGAAGGAGC 480

GTGATGATGC GAACTTCCGC TGAGAACTAA TTATGGAGAG GCAGTGAAAT

530

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

TGCTCGCCAC AGGGGACATC ACCTACTCCC TTGGCCTCCC ATCCAGTAAG CCTATGAAAG	60
ACCCCCAGAG GAGCTCTCGG GGATGGAGAA CACACGAAAG GCAGGATACG GAACACGAGA	120
ACAGCTTTAG GGGTATTTCC ATCAATGTCT GCCAACCGTC TCCTCACATT TTTGGAGATG	180
ATTTGTTTT CCCCAGGTAA AGTCTGTATT GCTGGTGAAT GCAGAGGTCC CTTGCTATGG	240
ACGGGCAGCT CCCC GCCCC TTCCCATCAT AACCAAGCCT ACTCCAAAGC TCTGACTGGT	300
TGATACCCAG CTAGCCTTCC TGTGAACACT CACCAGTCCT CATAACGTGA GTAAAGGATT	360
TTCAGAGACA CTTTAAGGTA AGGCCAAATG CGATTCTCT ATTCTACAAA AGGGAGCCCA	420
GAAGTGGTTA AAGAAGTTCA CTCAAGGTCC CTATAACCCA GCAACAGCAC GCACAGTGCT	480
TGGGCCTTAG GATCCTCAGC ACAGTTCCAG TGCTC	515

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

AGGACACTGT TCAACAAATG GTGCTGGGAA AATTGGATCT CTGCATACAA AAGTATAAAA	60
CAAGGTCCCT ACCTTATACC TTATACACAA ATCAACTCAA AATGGATCAA GGGGGGCTGG	120
CGTTGTGGCA TAGCGGATAA AGCTACTGCC TGCAGTTCCA GCATTCCATA TGGGTGCCAG	180
TTCTAGTCCC AGCTCTCTGC TGTGGCCTGG GATTGTGGGG AGCAGGGTCC ATCTCCCGCA	240
ACATGGTGGA GCACCCGGGA GACAAATAAG TACTGAGGCT GTGGACTGAn TGAAnCCTTT	300

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

TGnGAAAAGA GAACAGAGAC CTTAAAAGGT GGCTTGCCCA GAGCTGCCTG CTTAGCCTGT	60
GGCAGTCAAG GGTACTAAGT AGGGCTCGTT GCTCCCAGTC CAGTGCTGTT TAAAATTGCC	120
TCTTTGTGTT TCTCTTTCTT TTTCTTTCTT AATGGGCAGG CCACCTTTTC TGGACTGCTT	180
TTAAAGAATT GAAAGCTGAA TATTAGCAAT TTTTCAAAGA CACGTATACC TCTAGTTGCT	240
CCTCTTAAGT GATAAGTCGT ATCTGTTTTT TGCTGTAAAT AAAGTTAATG TGTCTACTT	300
AAGTATGTTT ATTCAGTAAA AATATTTGTT GAATACACTT TATCTTTATG TGTCTCTCTT	360
TACTCTTAAT AATAACCATG AGAATTGCGC TTTCACATTT ATTCAGCTTG TAGTGCATGC	420
CAGGCCTTCT GCTGAGTGCT ATGTCTGTCT GACTGTCACT TGGAACACAG TCCGTGTTCC	480
CTGTAGTCTA GAAAGGCAAG GGGACTTGAA GACTGCTGGT TGTCATAACT GAGTGCTGAA	540
GAATCGAGAC AGGACATTGA TAAATGATCA TTGAG	575

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

CTATTTCTGT TGACCAAATT TCAGCCAAAT TATACTCAAT CAGCATGCTT TCAGCAAATA	60
TCAAAC TCAA ATTACAGGCT GGTAATACT TAATACCTTG CCTGTACATT TAGTTGGGCT	120
AATAGATAAG CAGAATCAAC TTGGTAGGCA GAGTGTCCT GCTCCTAACT AACTGTGGT	180
ATGTGAGTTG AACGAGAGGA ACGTGTTTA TGTAAGCAGT GAGAGAACAC ACAAAGTGTG	240
AGGAAGAAGA TTTTGGAAGA CTACAAAGAC CAAACCCAGG AGAGGCCATC TCTAGCACCC	300
AAGGAGGTCG TGCGGAGGGT GAGTGTTGGT ACCATGACCC TGCTTACCGG CACCCAGCCC	360
TTGGCTnCCA TCTCCTCAAC CCCATCCCCT CTCCATTCCC ACATAAAGGG GGGAGAAAGT	420
CATTAGCAAA GTATCAGAAT GATAGCAGCA AGTGATGAGA ATGAAAGGAG AAGATGTTGT	480
AAGCAAATAC AGTGAGCAG TTAGCTGAGA TTCTCTGAGC AATGCAGACT CAGCCTGGAA	540

970

CCCCAGCTCC ACCACAAACC ACGGGAGGTC TCCCCAAGTC ACCTGTCTCT GAGCCTGTTT	600
CCTCATATGC GATATAAAGA CAACAGTATT AAAGCATAAA TGGTAATAGT TCTATTCCTA	660
CCTTGAAAAA TATTCTTGTA AGCATTGAT GTGATCATAT ACGT	704

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

GAAGCCACAC GGGGCTCTGA CCACAAACCC AGGCTCCTGn CCCCAGGCCT GGCCAGGCCC	60
CTGCTCCCTT CCCCCTCTGC AGCCCCGAC CAAGTGCCCT GGGCATGATT AGAGTGAGGG	120
AGTGAGGCCT GCAGACCTGC AGCTGTCCTG CCTTGCCCCA CGCAGCAGTT TGGAAGTTAC	180
CAAATGCCTT CCGTGACAGG CGGCCCCCAG GACCGCGGGG TCGGGGTGC CGCGGGAGTG	240
CGTGACAGAG GCCGGCTGTG TGACCCAGG CAGCGGACAC CCTCTCTGGA CCTGGCCGGC	300
CCCTCGCTAA TGGGCTCTTG GTCGCTCTCC TCCCTGCAGC CTA CTCTGCA ACCAACATGT	360
TCCCTGCAAA CCGTTCCTTT GGGATTAGGA CCAAGGGATC CTGTGGGCAG CTTT TAGGTA	420
CAGGTAGGGG CTGAGAAGCT GCCGGAGGGG GCTGGGAGCC TGGCAGAnGG GCCGGCCTGG	480
CCTGGGGGGC ACACGGAGAG GAGAAAGGGA nCCTGC	516

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

CCACCTCCAG CCGTGTTCAA ATTAATCTTG GCAACTACCT CATGTCTGGT TTCCGTTGGC	60
AACCAGCCAG GCTCTGGGCA TGACCTCTC CAGTGGACAG CCTCTGCCTC CTGGGGCCTG	120
GCCGCGGCTG CCCACGTGGC TTTTGGCATG TGACCTGGC CTTCC TTGGG GTGATCCCGG	180
GGCCGCGGG CGGCTGGGG CTGGGTGCC CAnGTAnCC CAGCTCAGAG GGCTAGGCAA	240
AT	242

(2) INFORMATION FOR SEQ ID NO: 421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

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AGGGTACAGn GTCCTGAAGA CAGAACAATG AAGAAAACAT AAACCCTGTC CTGAAGGAGC      60
TTAACTAGAG AATCCCCTTG CAGGGTCAAC GACCAATCCC AAnnCTGTGT GTACAATAAG      120
TGGTCCCTCA AGATCACAGA TCAGGGACAT TCATCTTAGG TTGGGTGGGT AGGGAGAACT      180
TCCCAGGGAG GGGACCTCTA TGTTGACCCT GAATACTAAA CTAGCCAAAA AGAGCCAGCT      240
GAGAGAGGGA GGTGGGGACA GCTAGAAGAA GCATTCCCAT ATTTAGTGAC TACCAGTAGT      300
TCCATATGCA CCTAGCGGAA GTGAAAAGTT GAGGCTGGAG GAGTTGGGAG AGGCAGATCT      360
GAGTGGGTGT GGTTTGTCAG GTTGAAGACA GGAAGACCA AGGACAACCA AGGAGTAGCA      420
GGCAAGGGAG TGACGTGGTC AGATTTGAAC TTCAGAAGGT ACATTCTGAT TGTTTGATGT      480
TAATAGTGTA TCAGGGGAGT GCAAACAGCC AGGGGGACAT TGCAAGTGTC TGAGAAATGG      540
TGATGTCCCA GCATTCTGA CCCAAGTCCT GCCAGTGGGC AGGCCTGGAC ACGTnCCAGG      600
GAAGAACGGC AAGACCGAGG ACTGTCAGGA TGTCAGCGG GnGGTAAGGG G              651

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(2) INFORMATION FOR SEQ ID NO: 422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

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CTCGGGTCAC TTTGGTTTCAG TGGTAAATAA nCAGTGAnGG ACGCTGCCTT AGGAAAGTAG      60
GGCATCCGTG GGAGCAAnGA GGGGCTGCTT TTGGTGCCAG AAnCTCCCAG CCCCTCACCG      120
GTCTCTGTGC GGAAGCCCAG AGTCTCCCTC CAnCTCCCT GGTCTTACCT GACCTGACC      180
CCAACAGCAT GGCTGCCAAG TTCTGAAGAC CCAGGGAAGG TAAAGGATAT GAAACCTCAA      240
GGGCTACTTC TGACTCCTGG CCGTnGGGGA AAGGGATGGA CTGATAATAT CCTTAnTCTT      300
TTG                                          303

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(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

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TTTCCTAGAA GTCTCTCTAG GACTTCCTTG GATTGGCTAG ACTGGAGCCC CATGCCCACC      60
CCAAGGCCAA TCGCGGACCA AAAAAGAACA GAAGTACCCC AGCTGGCTTC ATGGACACGT      120
GATTTGACCC CTGAGGTTGG GTCATTGCTC CCAGAACTCT AACAGAGAGG GCAGGAAACC      180
AGCTGTGTCT GTGACAGCCA GTCCCCCAGT CCAGTACCAT CTAAAGTCAG AACACAATCT      240
GAACCATGCT GTCAGTCAGG CTAGGGACGT CACCATCGCT GGAGACAGCA CCCCTGCTGT      300
GACCTGTGCT GCCCAGTGTG GTAGCCACTC CAGTTACCTG AAGTTAAATC AACTCCCCGG      360
TCACACCAGC CACACGGCAG GTGCTCCCCA GCCCCACGTG ACGGGCGGGC TACTGCTTGG      420
GTCCAGACTT GGAACATTTT CTTCAGTGCA GAAAGTCCA CCAGTGAGCT CTGCCGGCnC      480
CCAnCCCCAnG CCCCCAGTAA TGAGGCTCCC GGGCAGCTGT GAGGCGAGGG TCTTGCTGCC      540
CATCAGCGAC ACCAACAncG GCTTCCCCCA GCGCAAACGG GACTGGCAAG AGGGGGAACC      600
CCCAGnCCCCG GGGAGCCTTG AAGGGCAA                                     628

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(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

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TGAGCCACGG nCCCGGCTTA AATGGAAAAT TTTACACACA CACACACACA CAAAAACCT      60
AATTTCTTGC TTCTCTTGTC ATATCAGGAG ATCTGGCAGT AGTGGGGTTG GATTnTGGGG      120
TGGTGATGGn TGnTGnGT GGGGGTnCC TTGAGCCATA ATGGCCACTG CTCTTCAGCT      180
CCCTACCACC CAGGATGCCA GGGGCCCCAG GGCACCTCTCT GgnTTTCCTT GCATTGCCAn      240
AGTTGTGTTT TTCACAGTAG AGAGACATTT CTCTGTGCTT GTCGTTCTAT CTTAGATAGG      300
GATTGAAAAC AAATCCAGAG GCAGCTATAT TTTTCTAGAA AAAATGTGGT CTGTGTGTG      360

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973

CATGCnTGCC TGGTCCCTGC GTAAACACCT GTGnTGCTTT CCAGGGTGTC TATCCCAGGC 420
TTTCCAnTCT GGCCTCTTTG TCACACA 447

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

CAAATACCTG ACCTCTCACC TCCCACATTT TATCATTAAG AATCTGAAGT CAAGAGTGAA 60
AGTAACTTGC TCAAAGTCCA ACAGATTTTC CGTTCATTTT TAATTAAGTA TAAGTTTGGT 120
TGTGTGTTAA TGGGTCTCTG TGCCATAAGC ACCTACCACA GTGATTAGAA ATGAAGGCAG 180
ATCTTGAGTC AGATTCTAAG CTCTACGGCC TCTGAGTACA GGGCTGACTG ATTCAGTGGC 240
TTTGTCTCCT GTTAGCTTGC TGAAATTGCT TGCTTAGCAG TGGACTGGTA GGCATTGTAG 300
CTGGAACGCA AGGACAGAGC CTATAACTCT TCTACCAACT CATGTCAACC TTGTGCAAGT 360
ACTGAGACAG CAGCTGGGAG AACAAAAAGA TACAGAGATA AAAGAGGGAT AGATAGCTGT 420
ACCTTCATCA TGGGAGTACA ATGACGGATA AGGGGAAATC CATCTAAAA TTTAGGCCCA 480
GGCAA 485

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

ATCTGTAC CGTGGTATCA GCTCCCTATA CTGTCTTTAC TAAACACAAA AAGCGTCTCT 60
CTGCGGCACT GGTGTCAAAG CCAGTTGAAT CCATGCTTGG GCAGTGCCGT GTCCTCTCAT 120
CTCCCAGTTG ATTAAAGTCT GTCCTCAGCG GGATCATGTG GAAGGCTGGG ATCATGTGAT 180
GAGTTGACAC ATAATGTGCC TTTGCCGAGG CAGTGGGGAG GGGAACAGGT CCAAGAAGTT 240
ACAAACTAGC TCAGAGTGTT CTCCGACAGC ATCTTAGAGC TTATTGGAAC ACACACACAC 300
ACACACACAC ATTCTGATTA ACAAGCAGTT TTAAGACTTC AAGAGGTGCC AAAACCCGGC 360

974

ACTACTTGAT ATTGTTGTTA TTTATTGGGn AGACATTAAC ATCCACGGnA GACAACCATA 420
GTTCACTGTC CCTGACCCAC TAAGCTGCTG CACTTTTCCT CATTGCTTTC CAGCCCTTGT 480
TCAG 484

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

AGCCTGCACC AGGGCTGTGC TGGACTGTGG CGGGGTATGC AGGGGAGCGA TGGGATGTCC 60
ATGGACCCGT CCGCCCTCCC TGTCTGTATT AAGTCAGCGT CATGTTGCTT GAACTAAAAT 120
AGCTGTGAGA AGCCACTGAG GAAGAAGGTT TACTCGGCTC ATGCTTTTGG AGGTTACAG 180
TCTGTGATG GGAGGCCCCA TTGGTCCGGT GTCTGATACG GGCATTGGAT GGTGAAACAC 240
AGGGCAGAGA GAACCACACT GGGAAGCAGG AGGCAGTGAG AGGCAGGGAG CCTGCTCGTC 300
ATCTTCTTCC ATGTGGCTCT CCCTGGAGAG CACCAGGATT CCATCACAGG ACTCTACCCT 360
ATGGTCTGAT CCAATCTAGT CACTTTCCAA GGCCTCCCTT ATACGCATCG CAAAGGGTTA 420
ATTCCAGCCT TGACCCTGAn TCTGGTGAGC AGGTCTCCAG CACACAAGCC TTGGGGGCCA 480
ACTGGACTAT TATCCAATCC GTAGTACTGT CCCCAGACAn AGCTGGGCGT GCTCTGnCTT 540
CTGCGGTGAC A 551

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

TGCCCTCAGG GCCCACGGTC AGGCACAGCT CCTCCATGAA GCCCTCCTTA GCCACTCAGC 60
CGTCCCTGCT GTCACGTCAC TCCATTCTCT CAACAGACCT CACCCCTCCC TAATGTCTCC 120
CTGGCTTTGA ACTCCAGGTG CCCTCCTTGG TTCTCCTGGA CTCCAGTCTC TGGGTTGACC 180
TCAGCTCTGC CAACCACATG GGCTCACAGG GACCCGTTCT CTGTAGGTCC CACCCCTCAGC 240

975

TTCCAGAAGC CTCTGGGTTT ATAGGCTGAG AGTAAAGACA AACTCAGAGC ATGCAGGAGG	300
GCAGACTGAC AGTATCCTGC TACGAACCCA GCAGTGTAGC CCCGAGAACA CCTCAGGTGA	360
AGGCCAGAAA GTCTCCTAGT GCAGTAGCCC CTGCACCTCA GACCTTCCTT CTCAAGTGAC	420
AGTCTCTCTC CAGTGTCTCT CAGCTCAGCT GCTCTTGGCA AAAGCTTCCT GAGCCAGCTG	480
GAGCACTGAC AGTACCAAGC TGTTTCCAAG AGCATGAGGG GGTGTCGGCA G	531

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AAGAACTTGG CTTTGTAGGA CTGATAGTCT AACTATGTTT TCTAAGAACT AGAAAATGCT	60
TATATCGCCA GTACTCGAAA ACGTGTATGT GTTGATATGA TGTGTGTGTG TGCGTGCAGA	120
TTTTGGATTT TATTTAAATA TAAAATGCAA ATTTATTTAC TCTAAGTTGA ATCTCACTGA	180
AATGAAAATG AAAAGGCAAT ACTATTCCTT TAATATGGTT CACTAACCTT GTTCACACCG	240
TACTGATGC TCGGTAnGGG TTGCCGACC CCAGTTCTTC TCAACCCTTG ATGATTATGG	300
AGGATTAATT ATAATTGAAA ATGTGAAAAA AAGAGACTAG ATCTAATCCA AAAATCAATT	360
TGGCATAGAA TTTAATAAGA GATAAAAGCT CAAAATTCTA TAACTAACAA ATGAAAAATA	420
TCAACACGGG AAAAAGGAGT TTAGTTCCCA GCATCCAGGC CCGTACCGTG TGGATGCCTC	480
CTGGCCTCTG CTCTTCATCA GCTGCGTGAC AAAGGCACGG nCTCAC	526

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

AGAAGATATA TGAAAAAGCC TCTTGATTTT TAAAATTTAT TTATTTATTT ATTTGAGAGT	60
GACAGAGAAA GATAGATCTT CTATGCATTG GTTTAATTCT CAAGTGGCCA TAACAGTCAG	120
GTCCTGGCCA GTTCAAAGAC AAAACCAGGA ACTTAATCCT TCCCTTGAGA GGAATACAAG	180

976

GATCCAAC TA	CATTTGCCAT	TGTCCACTGC	TTTCCCATGT	GCACAATCAA	GAAGCTAGGT	240
TGGAAGCAGA	GTATGTAGAA	ATCTAACTGG	CACTCTGCTA	ACGGTATTCC	AGAGTCACAA	300
TTAGTGTTTT	AAACTACTGT	GCCACAATGT	CAGCTCCAGC	CCCTTAATTT	TGATAGAAAT	360
GTGATAGTTT	TAGAATTATC	AAATTTACAG	ACTATGCCGT	TGTACAAAAT	TGCTAAATAT	420
TAAATATCC	ATTTTATGAA	GAGGTCCAAA	TTTGATAAGA	GTAAATAAAG	GnAATATATA	480
TAAATGCAT	ATAGTGAAAG	GAAAAATT				508

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

AGAACAAATT	AAGTTCCTTC	TTATTATCTT	TCAACATTTT	AGTTTTACCT	CAAAAATGGC	60
TTACTTCTAC	TGAAAACAAT	TTTCTTTATT	TCTCAGAATT	AGGTTTTTGT	AGACACACAT	120
CTTATTTTTT	ATTGAGTTAC	TAAACACTTG	AGCTCCTATC	TATTCAATGG	TAACCCACTA	180
GAAGGACAAA	ATGTATAAGA	CTAATAATAA	ACTTGCCCTG	AAGATTAGAA	AAATTTATTA	240
ACTATTTTTn	CTTTTGTTGT	TTAATGCCCT	AGTGAAATAA	TTTCATGTTT	CTAATATACT	300
ATAGTGTTGT	GGTnTGTGTT	ATTATATGGC	ATACCAATAC	AATTCTTCAA	AAGGCTATCA	360
CAGCCATGCT	GATCATTTTG	TTTGGATGAA	TGGGTAATTT	TCAGTGGAGG	TAATGCAnAG	420
GTTTCCCAT	ATTCATCATC	ACAAAATCAC	ATCTTTACAA	TCAGAAT		467

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

TGAAAAC TAC	ACTGTATTTT	AGGAATGnAA	AATAATCTTG	GAGCTCCCTA	TCTTGCCCTTA	60
TGTAAGATAA	GCACTCTGTG	TGACATTGTC	AGTTTTTAAA	GAGCATATCA	TATAGAATCG	120
ATTGGTTCTC	TCAGTAGAAC	TGCCAACTAT	GGTATTTATT	TCATGCCTTC	ACATCACTCT	180

977

TAGCAGGTCA AAAATCATTG TCTGTGAAC ATCTAAATTG CTTCTTTTAT ATATTTATAT	240
TAGCAATACC ACTGAAGGGC AACCCCTAGA TTCCGTGGAC ATATGGGTTG TTTGGCATCG	300
GCATCTGTCA GTTCATTAAT CACTAAAGAA AATTTGGCTG AATTAATTTG TTTCCGGnTA	360
TCCCTTTATA GTCGTGCGTA TTAAGTCCTT ACCAGATACC ATCTTAGGCA ACCCAAGACA	420
CCTTCCAAGA TAAGAGTTTC ACCATAGTTA GCAAAGTCAG AGCnAAAnGT AACATC	476

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

TTTTTCAGAC AGAGAACACG TAACGTTATG TGGAAGACGG GGTGACAGCA GGGATAAAGA	60
GATACTCCAT GCTCTGGTGC TGTGGCACGC CGAGTGAAGC TGTTCCTCT GATACAGGTC	120
CAGTCGCAGC TGCTCCGTGG CTTCCGACCG GCAGCGCCCC GGCTGGGGAG TGAACCAGCC	180
AATGGAAGCT CTCATTCTGT CCCTTTCGAT CTCCCCTCTG TCACCGTGTG TTTCAAATAA	240
GTGAAATAAA CCTTTCAAAA AGAAATTTTA TAGAAACACG ATGAGATTCT TTTTAAAAAC	300
AGTTGTAGAA AAACCTTGAA AACTTGTAAT GCTAACCAAG ATGGAGAAGA CAAGATAGAA	360
AAAAGGAAAA GAATAAAAAG GTATTTAGAA GAGAGTGAAA AGCATGGACA AAGATTGTTT	420
TTTCTTTTGT TTTTCTTCTC AAAGTAGTGG AGGGAAAAGA GAGAAATGGT GAGATGTAAT	480
AATGAGTACG AATACGGTTT GTCCTGTCTT ACTCT	515

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

GGATCCATCT TGCTACTGAT GGTAGCAACA GTACTTGCCA ATCAGTATGC ATTGAGTGCT	60
TACTGTATCT GTGCCAGTCG CCAGGCTCAG CGCTTGAGAG ACACAGCCTC CCATTAAATG	120
GTAACGGACT GGCAGGACAC CTGCTCTTAA ACCTAGAAAG AGATTCACCA AACTTCTGTG	180

978

TTCAGGAGCC CAGCAGAGAG TTCAGGTCAG GAGGAGCCTG CCCACTCCCC ACGTCCAGTT	240
CTTTTAAGGG TCTCTATCTT ACTAGGGCAG ATAAGGAGGA AATGAAGGCA GGTGAATAGT	300
CCCTGCACCC CAAGTGGACA CTTTGCATCT CTAAGCAACT CACCTGTGTG CAGAAGCTTG	360
TGGCATTTCCA GAAAGAATCC ACTTTGAGCT CACCTCTCAA GGGGACACAG AnGCAGTGCC	420
TCCAGGTCAA GCAGTGGAGG AAAGGGTGTG GGTCTTGGAG CAAGAGAAAA CTCAGGGGAC	480
TATGGCCAAA CGGGGGACAC TGTCCTTC	508

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

AGCATAATCA AGGCGATTTA TAACAACCCA TGGCCAATGT CCTATTGAAT GGGGAAAAGT	60
TGGAAACATT CCCACTGAGA TACGGTACCA GGCAAGGATG CCCACTCTCA CCACTGCTAT	120
TCAATATAGT CCTGGAAGTT TTAGCCAGAG CCATTAGACA AGAGAAAGAA ATTACAAGGG	180
ATTCAAACCTG GGAAAGAGGA AGTCAAACCTA TCCCTAGTTG CAGATAATAT GATTCTATGT	240
ATATGGGATA CAGAAGATCC ACCAAGAGAC TACTGGAACCT CATAGAAGAG TTTGGTAAAG	300
TAGCAAGATA TAAAACCAAC ACACAAAAAT CAACAGCTTT GTATACACAA ATAACGCCAC	360
AGCTGAAAAA GAACTTCAAA GATAAATCCC ATTCACAAAA GCCACAAAAA AACATCAAAT	420
GCCTGGGATA AATTTAACCA GGGTGTCAAA GATCTCTATG ATGAGAnTAC AAAACCTTAA	480
AGGAAAGGAA ACCGGAGGTT ACCAAAGGAT GGGAAAATCT TCCnGTTCC TG	532

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

CCTTCGTTCA AGCAAAATAT TTCCCGTGGG AATAACTTCA ACACCTTGGG ACTGCGTCAT	60
CCTTCCCTAA CTTTCATGAGG GAACCTTGGC CAAACTGCTT TTCGATCTGG AGGCGCGCCG	120

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CCTCCAAACG CCTTCATCTT TTCTTCAAAA GAAGAACTAA CGGGAACATC CCCTTTAAGG 180
 CTTTGTGACAC CACAAGCCTC CCATGAAAAA CCCCgcGCAA GgNCAAGAG ACGCGCTAnC 240
 A 241

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

CTTCTGATTC TATCTCTGTA TTGGTTATTG GTCTGTTTAG GTTTTCTATG TCCTCATGGC 60
 TCAATTTAGG TAGATTGTAT GTGTTcAGGA ATCTATCCAC TTCTTCTAGA TTTTCCAAGC 120
 ATATATCTGT AGTTTGTGAT TATTCTTTTT ATTTCTGAGT TATCTGTTTT TGCATCTCAT 180
 TTTTAATCTC TGATTTTATT GACTTGAATG TTCTCCTTTT TTTTTTTGTT AGTTGGGCCA 240
 ATGGTTTATC AATTTTGTG TTGTTGTTTT TCAAAAAAAA GCTCTTGATT TCCCTGATCT 300
 TTTGTATTGT TTTTGTGTTG TTCAATTTT GTTATTTTTT TCTCTAGTTT TAATTTTCTC 360
 TAATTTTGA TTTGTTTCT TCTGTTTCT CTAGGTCCTT TAG 403

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

TGGCTCTTTC TACAGATAAA TGTATATTCC AGAGAGCATT TTTCATTTAT CCTTACCTAC 60
 TGACAATCCT TATACTCTGG TATATGCAGT GAATGTGCAA GTCTCCTCAG AGGAAACAGT 120
 CAAGAATGAT AGGAGCATCA GTTACAGAAT TTTCTGCTGA CATATGTGAT ACGATTGGGA 180
 GAGTACCTTT TCTCTACCTT CTAAAACAAA GAGTTAATCA TAGCCATTAA TTTTGTAGCC 240
 AGTGCAACCA AATCACGAGC AGCTCCAGAG TCAGTTTTAA GATCAACTCC AGAGGAAGAA 300
 ATCCCGTAAC AGTCTCCCTT CTCCATCCTT CCTCCCCCAT AACTGGTGCT TGCAGTGCAG 360
 TCAGAACTTC TACAGATCAC AGACATTGTT TGCCCAAGCT GACCAATCTC TAAGGCGGGT 420

980

TTTTCTTCCC CCCTTCAAGG ATACTTCATG TTAACAGCTT GAGGGCGTTC AATCAGCACT	480
GCTTTGATCT CGGGCTGGAA CTATAATTAT TTAACATTGT TACAGGATTT CTATAATCCA	540
CCCCACCATT AAATCCCTTT TACACCCTCA TCTTCTGAGG CCTAAATCTG GCATCCGTAn	600
ACTTGGTTTG TCT	613

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

AAAAGAAAAC TTCTTAGAAT TCCACATTCC TCAATTATCA CCAACTTTTC TATTGCTTTT	60
CTTAGTAAAA ATGTTTAAAG TTCTCTGAAC TTATCCATAT CACTCAAAAT TCTATAGCAA	120
CCACCTATTG AAATGGTTC TTAACAAATT CAATTATCAG CCACCTGTAA ATCATTCAAG	180
GTCATTGATA TAGTGAAATA TTTTCTTGCT ATGACCCAGG GAAGATACAA TCCTGTTTTT	240
ATTTCCAGAA AAAGTTATCA CTGCTAACAT TTTTGCAAAA GAAAGAAAAT GAAGGATTTA	300
GTTTACTTTT TTTATCCTGA TCACATAAAC AATTTTCATC ATTCATTTGT AGCAGACTCC	360
TGCATTAAAA TCAATTAACT GAGTATTTCA TTTAAAAACA ATGGAGAAAA GCAATTAGCC	420
TACTAATATA GACTGCATCT GTTGGTGAAC TAAAGGTAGA TATTTTGCGC CTCTGGACAC	480
ATTTTTGAGG TACGCTTGAT AGGATTTGTT TACAGACAAG AGAGGAGTTG TGAAAG	536

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

GGGGTAAGAG nGCCGCCGGT TTTTGCCCTG AAnTTTGAAT TGAATTTTTA AACCTTGAAG	60
AATTGGGGGG GATTGCAATT GCCCCTTGCG GTTGAATTTT TTGCCAGGTA ACAAGCCGGG	120
GGGGTTATTC TTCTCAAAG AAAGAnCGGT GGGTTTGThC ATGGAAAAAA GT	172

(2) INFORMATION FOR SEQ ID NO: 441:

981

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

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CCGGCACC GC AAGGnAAGGA TTAACCTACT GAGCTGTGGC GCCGGCCGAT TTATTTATTT      60
GAAAGACAGA GTGACAGACA AAGAGATCTT CCATCTGCTG GTTCAAGTCT CCAAACATCT      120
GCAACAAC TG GGGCTGGTCC AGGCTGAAAC CAGGAATTCC ATCCGGGTCT CCCATGGGTG      180
GCAGGCACCC AACTACTCGG GCCATGACCC ACTGCCTTCT CAAGTGCATT AGTAAGAAGC      240
AGGATCCAGG CTTTGAACCA GCACCTCTGAT GTGGAATGCA GGTGACACAA CCCCTGCCCC      300
CCAACAGATT TATTCTAAGA GGTTTCATTC TATACATTCT GACAAAAAGG GGAAAAAAGG      360
TGCCATTTTA GACTTTTTTT TAAGAAAGAT AGAGGTCTTG GTATGCAAAC TGTAATCTCA      420
AAAGAAAAAT AAAAAGCCTA AGGTTTTCAA AATAGTCCTT AAAAGTAATA TCATGACTTA      480
GCTTCTTTTT ACTGATTTGT ATTTTGGAGC GTTTCTAAAA TAGTTGCAAT TAAAGTTATA      540
TTTATGTATT TnAnATAAAT ACAAATGTAT ATAGTACATA TACTATACCT TTATACTTAA      600
AATATATATT CATTTAAGAA TGTGACACCA AGGGCAGGGC ACGG                        644

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(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

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GTGCACCTCA CAGGGGACCC ATGCATGCTC TGCCTGCGGT TCCTGAGCCT GTCTTTTCTC      60
TAAAGCACTG GCAGTCTCTG CCTCCCTGTC CTCTGCCAGC CCCACCTCTC CTGTCCCTCCT      120
CACCTCCACC TCTCCTTTTT CTCTGCCCC TTCTATGCCAT CACCATATTT TCCCTGCTGG      180
AAGCCCTCT CCCTGCTGTG TCTTTACAGC TGTCTCCTCC AGCCCTCTTC CGCACAGGAA      240
CCAGGCTGAG TCCCTGCCCA GAGAACCTGG TGTCAATCCC CCAGCTTAGC CAACGCAGTG      300
CACCACAGAG GCAGAGAACA GGGGTTGACC CTTCTTCCT CTGCCTCCCT TTTGTCTCCC      360
CACTACCAGC AGCTTCCCCA GAnATATCCC ACCTCCAGTC AGCACTGGGG GAnCTCCGCC      420

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AGGCCAACTC CA

432

(2) INFORMATION FOR SEQ ID NO: 443:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 630 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

TGTGTGTTAT TAAAGCAGGT TACTGATGCC TTGGGTTTGG TTTGTGTCTA ACCACAGGTG	60
GGTTTGGCTC TTTCCCTCTT CTCCCGTGTT CCCCATAGCA CATTGTGGTT TCTGGTGTGG	120
ACTCTGCACA GTACAGGAGT CTGGGGAGGG CAGCGAGTCC TGGGAGACCC TCACAAAGGG	180
CAGGTCCAGG TTCAGATGCT GGCTCAGCTC CAAGGCCTGT GTGGTCTTGG GAAAAGCCCT	240
TTAGCCACCT AGTTCTTCTT TCCATGCCCC CAGTGAGCAC GGCATCCACC TGCCTTTCT	300
GGTAGTGCCT CAGTGTGGTG ACACATGGAG CACATGTCAC AATGCTGACA GGGGGAGAGA	360
CGATTAGGCT TAGAGCCAGG GCAGGCCTTG GGTTCGGA AGACTAGCAG TGTCTAGGGA	420
TTTGTGTGCT GTGGCCTGAG GCAGTCGCTG AAGGAAAGTT CTGGAGGAGG GGTTTTGGGT	480
GTGGTCTGTA TATTGGAGTT CGTTTTTGGT GGGAGAGACT GAAGTTGAAG GTGGTTCATT	540
TTCTCCTTAG ATGTCTTCAG GCAAGTTCTC TGGCATATTT ATTTTGTGG GAAATGGCCA	600
AGAAGTTGAA AGAAGAGGCA GTnnCTGTTT	630

(2) INFORMATION FOR SEQ ID NO: 444:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

TCCTTTGATT TGACAACTTA TGATAGTATT CTTATACTAG TGTGAGCTA ATTGAGAAGT	60
ATGGAGCATA CAAAACACTC CCTCTTATCC CTTGTTCTAT AGGGAAAAAG AGGACATATC	120
CTTGATTTTT CAGGGGCTTT ATGGGAAGTC TCAGAGTTAG TTTTAGAGGA TATAAAAGTA	180
TCCTAAAAAT CATACTTTTA AAATTTGTGG TTCTGATCTT GAGAAGGTAA AATCAAAGGT	240
TGTTATATTT CTTACCTGAC TAAGACAGGA TCACTGGATT CCTGATATAT AAGACGTGGC	300

983

TATTTATTCA GCAAAAGATT CTACACAGTA TTTTAAAATG AATGTTACAG AGAGTAATAT	360
GA CTGTAAGG AGACTCGGGT GGGATATGGG ACCATGAGCT GGCCTAGATT CCTGGTTCCC	420
TTGAAGGATT CCATTTCCTC AGTTGTCCAG TAGCCAGnCC TTTAAncCTG GTGGGCT	477

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

CAAGAATCTG CCTCTGCCAA TGTCTGCAG CATTTACCCT ATGTTTTCCT GTAGTAATTT	60
GATGATTTCA AGTCTTAGGG TTAGTTCCTT CATCTATTGT AAGTTGATTT TTGTATAGAG	120
CATAAGGTAG GAATCTTTTT TCACACTTCT GCATATGGAG ATCCAATTTT CCCAACATCA	180
TTTGTGAAG AGACTGTCCT TTCAGAAGGG AAGTGCATTT AATACACTTT AGCTACTGAA	240
CACCGTAGTT AGTAACATGG TGCCTGTGG AGTACTGGTT GTTGCCCAT GTAACGTGC	300
TGTGGTTCAC TGCCCCTGCC AAGAATCACC AGAGGTGTTA ATACCTCATA TCACTAACCT	360
GGGAAAAGAT CAACATTCAA AATATGAAGT GTTGTTCCTA CTGAACACAT AACACTTTCA	420
TACCATGGnA AATTGAAAAA ATGTTAAGTA TAACCATTTT AAGTCAGTGA CCATCTGTCC	480
TGGAAACCCn ATAAAGATAT AGTAAGTG	508

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

ATGAGAAAAG ATTGGCAATC GTTTGAGGAC CTCCTGATAA CAGCGATAAA AATCGTCATG	60
CTTATTACAA TTCCTGCGAC ATTTTTCGTG TTATTTTCAA GTGACCGTAT CATAACGCTC	120
GTGTATAAAA ATGCTATTTT TAACGAACTA TCCGTGCGCA TGACCGCTAC CATATTTCGA	180
TGGCATAGCG TGGGAATGCT TGCTATTGCG CTGAATCGCG TTCTCATCTC CGCCTTTTAC	240
GCGCAnACAA CTCTTTTGCC CCTATGATTG CAGGAACTAT TTCATTTGTG ACAAATATCA	300

984

TTTGTAGCAAC ACTGCTCTTT ATTCCCTTAG GAGGTAAGGG CATTGCATTT TCTCTGAGCG	360
CGGCGAGTAT GGTACAGACC GTTTTTTTAT GGATGTTTTT AAAACGATCG TGGCAGATAA	420
CTATCCCTTC ACTGTATAAA ACTTCCCTTT ACTATGGAGT GAAAATAACT TTATTTTCTG	480
TAATCGCGCT GGTACCCACA TGGGCAAGTT CTTTTTTTAC GGCGnATTTT	530

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

CTACCTCTGC TTCTCAACAA CCCGACCTTG AGAAATCATG AACAGCCAGG GGACAGGCTG	60
TGCAAGGTGC TGGTCAGATT GGGAAAAGGC ACGGGCAGTG CACCTGGCGC ACGTACATTC	120
TGCACCCAC CCTTCACTCA TCCTCGGCTT CAGCCTTCCC TGTGCGGAAT CAGGGGCCCA	180
TTCTTTGAAG GGGGGAAATC ACAGGAGCAC AGTTCATGCA GTGCAAGCTG ACCAGGGAAA	240
CGTGCGGAGG GGGATTGAG CTCGGCCGAG CGGGTGCTGA CGTCAGAAGC AGGGTGGGCG	300
CAAGAGAGGA TGATTCTGGC ACATAGAGGT GAGAGGGCCA GGGCTCCAGG CAGCTCTCCT	360
GGCCACTCCC CGCACGGCAG GTCGGGGCCT TCCGTCTGCG AGATCCAAGC CTGCACATAG	420
CACCCCTCTT TTTAGCATTT CCCCCACGAG GCTGACGATT CCTGTGGCT TCTGACTAA	479

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

CCATTTCCAG GGCCCTCAGC CTGCCCTAGG CCCACAGGCC TGCCACGGAG GCTGTGGCCC	60
ACTCCTCATG GTCTTCGGTC CCCACAGGGC TGAGCGCTGA GTCTGGCACC CGGTGGTTTC	120
TGAGTCTGCG GAGGAGTTAG TGGTGGAGGG AATTAAATGA ATGAGAAACC CGCCCAGGGC	180
CTGGGATTGC TGCTCTCCCT CCCCCTACAG AAAGCCTTGC CTCTCTGGCT CTCCGGCATC	240
TCAGCGTCTA TGATTAAAGC TTAAATCCCT GGCTTAGGCC AAACGGGGTA CCTGGTAAAG	300

985

AGGAAATCCT TTGGCTCAGT CTGAGTCCTG ATAGAAGGTG CACTCAGGAG GTTTCCTGA 360
AAAGCGAAAG AGCAAGCAGG GATTTGCAGC GAGACAGGGG GCGCG 405

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

GGCAATGTTT TTGCTTATTC TTGTCATCAG ACAAGGGCCA TTCTCTAAGG GTTTTGATAG 60
GCAATCATTG AGCATCCACT TTACAGAACT GATTTGGCTG CTTCTAACTT CTTCTTGTTT 120
CCTAATCCTT GAAAACCTCT AAAGACATCT ATTTTCTTTC AGTTACTAAA ATGTAGACTT 180
CATTGACCTA GTTAAATTCA GGACCCTCAG TTTTGTGAAA ATGGAGTAAA TGAAGTGTGTG 240
ATTGCTAACA AAAGTGTCTT AAAATAAGAA TGTATTTTAT TGTAAAAAA TTTGCAGACA 300
TATAAAATTT GTACTGATTT GGGAGTACTC TGTGACATTT TGATACAGCA TATACCTTGT 360
GTAATATCCA ACCAGCATAG ATATATTTAT CTCTTCAAAT ATTCAACAGT TTTTATAGTG 420
GAAACATCAA AAATGATATC TTCTAGTTCT TTTAATAGAG AAATATACAG TACATT 476

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

AAGTGAATTT GATCTCTTTA AAGCTAGGCT AAGTTCTGC AGCAGCTATT CAAGGGGAAG 60
GCAAGACACA CTGACAATAA AGACACGTGT ATTCATTCAT TGGGGTGACC GAATGACAAC 120
AAAGCAGATG AGCCTATAAG AAAAAGCCAT TTGAATGTGA TAGTTGAAAA TCTCTTGTAT 180
TATCTTTAGG GATATCAGGT TCATCATACA TGTGATGTGT GAGTGGATAG TGAAAAAAG 240
TTATCCTTTT TAATATTTGT TTCTCACACT TGGTCTTCT TATGTGTGTG TGTATGTGTA 300
TGTAAGCTAA ATTAAGCTCT TGTCTGTGTA ACAGAAAGGT GGGTAGATGT GGTTAGAATT 360
TTCTTTTCC TGTCACTT TCTAAGGATT ATTTTAAGA AATGGTATCT ATTTATGTCA 420

986

TGACTGATAA GTATTTCCTT AAGTATTCAC TGATATTTCA AAATTTAAGA CTTATGCTTA 480
ATTAAGAAAA GGATGAGAGA TCCAATTCAA TCAACCCCAT TTCTGTTCTA ATATATGAGA 540
CTTCGGTGGC TAGTGGATTC CCTCATATAA G 571

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

AGGTAACACA GTAAAGGATA AATCTATATG ACCTCTCAAT ATATGCAAGA AAAGAAATAA 60
TAAATATACT GCCCACTCAC TGTA AAAATG AGTACCATTA AAAGACATCA AAACCAAAT 120
CCCATTGTGT ATCCATAGCA CATAAACAGG AAACAAGATA TCCTCACAGA AGCCAAAGGA 180
GAAAGGAGCA GGGGAACAAT GCGAAAACAG CTAGCTACAT GCATCAGGAC TTGTGTAGGA 240
CGGAAGGTGA AAGACTACTT ACTGGTAGGA GAAATTATAG CTAATTTGCA GCCATGTTTG 300
TACCCAGGAT CCACTCCCAT CAAGTACGT CCTGGAACAG GGCTTGTTAA AAGAAGCTGG 360
ACGAAGGTTT CCGTCCAAAC ATCATTACTG ATTCTTCTC TGGCATCGGG AAGTCAGTTT 420
GGGCTCTTCA AAAATATAAA AAGAAAAGAA TTAGTGAGT TTTTTCATTT ATCCAAGTTT 480
TCTTCCAGA AAAAGAGAAT TTATTTTGTA TAGTCGGTCC TTGCAGGAAC ATTTATTATA 540
ACAAAATGAC ATAGTAGAAA AGCAACATAT AATAAAATTA TATTGTCTAT TTTTGTnAA 600
TCCCTGTAAC ACATGGCACC ACAACAATT CTGA 634

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

TTAGTATCTG TGGTCGTGTC ACCTTACTGT GTGAATGACA AAGGAGTAGA TGTGGAGAGT 60
GGATTAGGGT GAGAAGGTGT AATTGCAGGT GAAGGTGAGA CAGGCTGGAA GGAGTCACAA 120
AATTGAGCAC TCTTGACCTG ATATGTATTC CTCTCCACC CTAACATATG TCTGTCTCTG 180

987

ACAGAGCACA GCCTGCTCCA CTTAGCTCCA AACCAATCAG GAGCAAGGAG TGTACACACT 240
 CTGACGACAA AAGACCCAC CTA CTGCTG TGCCTTGTG CCAAGCAGCC TAATGCAACT 300
 GAATTGTGAC CTTCTTGTGG TGGCAGTAGT GAGCCACACT GTGATTTTGA GTGTGTCTTA 360
 ATGTAAACA ACAACAGAAC ACACAGGTAC TCTGTGCTGA AGAGGGCAAG CCAGAACACT 420
 GAGCTGGGAG CAGACTAAAG TGCTGTATCC CAAGGGTGTG CTGCTA 466

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

AGAGACCAAG GGAATTATTT CAGCAGTGTT GCTCCATGGA TCAACCAAGA GACAGAGACA 60
 GAAAGTGGAA ATCACCATTT GCAATGAGGC AGACACAGCA GAGACAGAAA GGAAGGATGG 120
 GTGTGAAAAT GTGTAGGAGG CAAAGTGAGC AGGACTTGGT GGTGGCTGG AGCGTGGAGG 180
 TGAGAGACAG AAGAAAAAGA AAGAACTCAG GTTCCTGAGC TGTGCAATAG GATACATGGG 240
 GCTGCACTTC CCTGAGCCGG GGCTGTGTG AAAGGGGTGG AGATGAGGGT GGGAGAGAGT 300
 GGAGAGAAGA TATAGTGATG AGTATTGACC TGGCACACCG TTTCTTCAGG ACACACACAG 360
 GGAGAACATA GCCATTTCTG TACCTTTnCG CAAGCCAACA AGAGGGAATC ATAATTGAAT 420
 TTCCATGAAT ATTTAAACT GAAAGGAAAA GTCTGAACTA GAACTATCAT TTACAGTGAC 480
 TATATGTCAA GATTCTTGCC AGCCTTGTTA ATTTTACATA TGCCTATTT TACCTACAAA 540
 TTATATCTAC TCTATCATTT TTCTCAAGA ATChATTGnT ATTTTTTAAA GATTTTATTT 600
 AnTTATTGAA AGAGATACnC nGAGAGAGAA A 631

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

CAGAAGATTT TAGCTTTCCC TGGACTTTAA AGTAAAATTG GGCAGAAAAA TGCATTGAAG 60

988

CAGGATTTTT TTAATATCTT CCCGTTTAAT GTTCTCTAGT CAAACCACCA AAAGAATGGT 120
GAGCAGTAGA CAATTGTCCA CATCTCCCTT TGTGTGGTCC CTTCGTTGTC CTTGATGAGT 180
GCCTACAGAG AAACCGTAAG ATTCAAAAGC TGAGCAGAAA TACTCTGATA CAGAGAGGGG 240
TCGTAAGTTT CCCTTCATTG CTTCAATTGTG GTTCTACAT CAGACTGCAG CATATCGTTT 300
TTAGAAGTTC TGTGGTTTGC TCTGGTAGGA CTACTCCCC CGTCCTGTTA CTCGAGAACG 360
TTTATCCAGC GATGAGTACT TCGGTGTTAG GGATACTCAA CACAGGCCCC GGGAAGCAAC 420
GGGATGATAT TTTTGGCTGG CACGTATCAT TTTGTGTACT TATTTTCCTA TCTATTCATA 480
TTTGACGAGC CAAAAGGGGT GAGGTAGGAT ATCCTATCTG CTGGTTCACCT CCTCAAATGC 540
CTCCCAACAG CCAGTGCTGG GCCAGGCTTA AGTCAAGAGA TTGATCCTCA ATCCGAGTCT 600
CCAAAGTGGG TGACAGGGAC CCAAACACTT GAGACAT 637

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

AGTTCCTAAA TGAAAATCCT TCTAAACTAA GGTCAATTGCC TTTTAAATG GAGGCCAACC 60
AATATCACGA TTAGTGCCTC TCTTCTGCTT CTGTCTCTCA TTTCTCTTCT TCCTTTCACT 120
TAATGCCTAC ATCATGCTCA CACACAGACC TCTTCTCTCC ATTTGTTTGT CACAGAAGAG 180
ATATCAGTCA GGGTACACCT GCAAAAGCAG AAGGTGGGTG CTTGTGCTCC ACCCATCCTG 240
CAGTTTGTAC CTGAAGATTG AAGACATATT TTGCGAATGT TTACCAATGT CTGACACATA 300
TTTATACAGT TAGCAAATAG TAATCTGAAC CATGAAAACA TTCCTAGAAT ATTTACACAA 360
AGTGAACCTCT AAATAGAATT CTCGGTCTCC ACCTGAATTT CATACTCTG GATTCCTCT 420
ATGGTTTCCG AGAGAACTCC ATATCTTTCC TGGGGTGAGT TCATT 465

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

CAnTACTGTT TGCATAATTA GAAATATAG CGTTCCATG TATGTAGCTT TGACATTATA	60
AACTCTTTAA GATTACCACA GTGGATGTCT GATTCTCCA CAATGTGTAA ACGGGCTTGG	120
AAGTTGGCAG ACTCAGTCTC ACAACATGAA AAATATCTGA ACAAACTGAA AATCAATGAC	180
TTTTGTTTGA TCCCTCAGAG AATTGTGGTC ATGAGATAAA CCACTACCCT GAAATCTAAA	240
AGCAGTAGAC AAATGGAATC ACAGGTGAGA TCAACTCAAT AGGGGTAAGC AGACAGAACT	300
GATAACTGCT AGGAAAATCT AACCGGTAAA TTGAAAAAT CTTAGAGACC GAACTGGACA	360
GTTAAAAGAT CCTGGAAAAC CCAATTTTAG TTGGACCACC AAACCCCTAT CTTGTGGTTG	420
GCACAATGAG GGCAGAnGGG TGACCCTCCA AGGATCTCCT CCAGGTCTC ACTCTAACCA	480
TCTGGATAAA ACTTCCCTCA GGTGTAGACA GGGTGGGAG GAAATGAAAC ATTTGAGATG	540
CGCCCAGAGT ACTGGCCACn ACAAGACCT AATTCCTAA GGGGAATCAC TCAGAGCACT	600
AATCTGGCnT GCAGAAAGTT GGGGG	625

(2) INFORMATION FOR SEQ ID NO: 457:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

nTATCGTAGG CAAGATAGAC ATCCGTAGGA AACACCGTGA GTGACAGTTG CCTGTAAGnA	60
CATGGGACAT GTAACCTAGC CTAGCGGTC ATGATAGAAA GTGCACAATA AAACCTCCAG	120
GATCACATCG GCCTCCACGC AGCGCCTCTG TCTCCCCCGC CCCGGCnCTG GCCGCGAGCG	180
GCTTCCCAGG CTGGAGCTCG GCCAGGCCCC GCGGCGGCTG CTAGGGTCTA AGCnGACCCG	240
GGAGATGGAn CGCAGACACA GCCCCTGCCG CCTGGGGACC CG	282

(2) INFORMATION FOR SEQ ID NO: 458:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 531 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

990

GGTTCAGGCA ACTCAGGCCT GTGTTGTCCT GCACCTGGGC CTGCAGCTGT CCCTCCAGGC	60
TCTCCAGCTC CTTCTGCAGC TGCTCAGCCT GCGCCTTCAG CTGCTGCTCC GCCGCCGCCG	120
GCCCCTCAGG GGAGGCTGGG GACTCTGGGG TGGGAGGCTC AGCTGAGAAA GGAAGCAGCC	180
ATCAGGGGCC CTGGCCTCTG GGTTTTCAAA AAGCTCCTGT CTTGGTCCTT AGCTCCTCAG	240
GCCAACTTCT TGCCCCCACC CCGGTGCTGG CTTCTTGGCT AACAACTTTC CATATTTCAGA	300
TGGTCATTAC CCTTCCAAGC CAGGACACAG AGTGCTTGAC CGTGGCATAG TGGACAGTGG	360
GTGCGCCACC CCTATTTACA GATGAGGTCT CCTATGCTCA AAGAGATAAC AAGACTCGCC	420
ATCCACCGGC ACAGACCTGC TTCCCTCTGC CACAACACCC CTCAACGGGG CAACCAACAA	480
CCATCTGCT CCCAGGCCAA CTCTGCCCTG CTCAACCATC TGGCTCTTGA G	531

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

CCACCGTGTT ACCTGGAGTT GTAGCGCCCC CTGGTGCTAG TCTAACTAGC ATGGCACCAA	60
CTCAGGTTTG CCTCCGTCCT TGTGCCTGCT ACCCCTGTAT GCTTGACCA TCTCCCTTCC	120
CAGAGGACTG CGCCTGCTGT GCCTTCTCTT CTCCTTTCTT CCGGCAGCTT GGTTCCCAAT	180
GTGAGGCACC CTTCCCGGCA CTGGGGTGGG GGAGGCCAAG ATGGGGCTTT CTCTTGAGCT	240
TGTGGCAGTG GCAGGTTGCT GGAAGGAGCT GGGCTCCTGC CACCCCTGGG CCAGTACCAA	300
CAGCTGGCAG TAGCCCTGGA CTCCAGCTAT CTAACAAACA ACTCAGTAAC ACCATAGAGG	360
AATTGTAAG AGCCCAGTGG GGTCCCCTGA TTCCATGCTG CCCACCCTGG GCTTCTGTTT	420
CCCCGTGGGC TCTGAAGAAA GGGGCTGGGG GCCCCCTGGT GCTGAGGGAG ATGGGGTGCT	480
GGGTGGGCCA GGTCTCAGTG GAGGGACCCC AGAGCATGG	519

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

AGATTTTTC	CTGTCACTAT	GCAGGGGGAG	GTGTGTATGT	GGCTATTGGC	ATCTGTAAGT	60
AGAGGCCAGG	TGTGTCTCTA	AGCATCCAAT	AGTGCCTAGT	GTAGGCTACC	CCTCCCAACC	120
CCCAAGTCTA	CAGGCCTGGA	ATTGAGACCC	TTGAAAAGAC	CATTATAGTC	CATATTTAGG	180
AATTTGGGCT	GTAGCCTAAA	AGTAGTGGGA	AAGAACTAAA	GGGATTTGTG	TAAGGGTGCG	240
ATTTGATTAA	ATTTGTGCTT	TAAATTTTTC	TTTCATTTTA	TCCCTCTAAT	TTGAAAGGCA	300
GAGAGGGAGA	TCTGCCATCC	ACTGATCCTC	CCACCCCCAA	TTCTTGCGAA	CATCTGGGGT	360
TGGGCCAGGC	TAAAGCCAGG	AGCCTGGAAC	CTAGGTCTCC	TACTTGGGTG	ACAGAGACCC	420
CAAGCACTTG	AGCCACCGTC	TGTTGCCTCC	CAGGGTCTGC	ATTATTAGAG	AAGTCCAGAT	480
AGTGTGTCCC	TGGTGGTCCA	GTGGCCAGGA	TTAGAGAAGG	CCAGATAG		528

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

AAACTGGCTG	nATTTCATGTA	CTAATGnCCC	TTGAAGGAAT	CCTAAATGAC	TAAAATCACA	60
ACAAGATTTG	CTCTTTCAAG	AGATTTGTCT	AATAAGnGCA	GAACTGAAGG	GTTTTATTTT	120
TTAACCAGAT	AGAAATGGAA	AAGCATTAC	TTTTCATAAA	TGAAAAAAAT	AACTCACATT	180
TCATAATCTT	TTATGAATGn	TGTGGATCAA	CACTGAGAAC	ATTTCAAATA	AAAGTAATTC	240
TGCCTCCTAT	GGAGTTATTT	TTTCAGATAA	ATCCAATCTG	TACAGAACCA	TCTGAACCAA	300
ACAnATGGGC	TAATACCAA	AGTATCCAAG	TTAAGAACGA	CTCTAGACTT	GACCTTGGA	360
ACnTGGTGAT						370

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

992

TGCAGCGCGC GGCACACGGG GCGATACAAA ACTCCCTCTG CGCACTGAGA ATTGCAAGTA	60
TAGCGCGCCC CCACCCCCCT GTCTACCTGA nGAnGGGGCG GGGCGTGCGG CGGTGACGCC	120
ACCCCTGCGCC GGTGGGCCCC TTCTGGAGGG TGCTAGACAC GGnnnGGGGG GGGGGTGTG	180
TAAAAATGAn ATGGGTCGGG AGGGAAGTGC ACCGTGCATT CThTTTTTGT GCGGGCGCCG	240
GGGCGCTGCT CCCGGGGTTT GGCGCACTGC CCGTTTTTTC TGAGCAGCTA GGCATTGCCC	300
CGCAGTAAnT GGTCACGCCC AGCTGCATGG GGCATTAAGT TTAAAAAGAA ACCTTCGGTG	360
CAACGAACGA nTAAACGCAA CGGTTTT	387

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

CACCTTCCTT CTACACCTAA CTTTTAAGGA TTATTTTAAT TTTGAAGAGA TGTTGAATTT	60
ATTGAATGAT TTTTTTCTGC ATCTATTGAT ATGATAACAT GGTTTTTGCC TTTCATTTTC	120
TTGACATGAT GTATTAGATT TATCAATCTC ATTAAATTC CTTAAAATCT TCTTCTGAAT	180
TTTTTTGAAA GGCAATTTTC ATTTCTTTTG TGATCCCTTG CAGGAGATGA TTGGGTACT	240
TTGAAGGTAT GATGTTACCA TGCCTTTTTT TTATGCTTTC TTCTTTTTTT TnTTTTTTnT	300
TTTTTGTCAT GCTGCTTTC CTCTTTCCGA TTTTGTGCC TCGCTGGCTC AGGTGCTTCT	360
ATCAGTGTTT TTAGCTGGT AGTAAAAGAT TTCGGCGGCA AGGGTACAGA GCATCAGTAG	420
AAGTGTCG TGGCTGGnTC CGGTGAGTAC TTTAAAGnGG CCAG	464

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

ATAGACATTG CAAAATGTCA AGGTACACAA TGGAAAATAA GCTCACATAT TTGTGCACAC	60
ACACACAGAG AGTAGGGTGG GTGGGGAGAG ATGGGATAGG TAGAGAGAGA GAGAAATATT	120

993

GATCTTCCTT CCATTGTTTC ACTCCTAAAA TGACTGCAAT AGCTGGGACC ATGCTAGGTC 180
 AAAGTTGGGA AACTAAAGTT CCTTCTAGGT CTCCCATATA GATGGAAGGG ACTTCGGTAT 240
 TTGAACCATC GTCTGCTGCC TCCTAGAATG CACATTAGCA AGAAGCTAGA TTTGAAACAC 300
 CATAGCTAAG AGTTGAACTA GGCAGTACAA AATGGCATGT GGGCTTCCCA GACAGTGGCT 360
 TAACCCCTTTG TGCCACAGTG CTCACCCTAA CATCTGCCAT TGTGACGCTC AGTATCAGCT 420
 TTGAACCAAG AGGAACTCTA CTCTGTAGGG AAAGGGTTAA AAAGGAGGCT GGTGGCAATC 480
 CCCAATCATG CCATAGACAC CTGAGGAATT TAC 513

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

CAGnAAAAAG ACTTATAAAC TGAAAGTTTT TTATACATCT ATTGTCCAAG AACCTGCAC 60
 AATCTAACTT TCCAATTATA CTCTCTACTT TCATTTTAT CACTTATATA TAGCCTTTTC 120
 AAGATTTTCTAG AATGCTAACA AAGAAAGTGA AATCACCCCTT GATGTCCAGA TAGTCTTAGT 180
 CCTCATCAAT ATCATCATAT TCATTTTCCT AAGTTTCATT CTTTTAACT GACACACAAC 240
 AATCACACAT ATTTACAGGA TACAATGTGA TGTCTGATG CATGTATATA TTGTACAATG 300
 ATCAAATGAG GGTTATCAGC CTACCTACCA TCTGTAATAT TGATCTATCT TTGTAGTGAG 360
 ATCAAATCC TCTATACAAG CTATTTTATA TATACATATC ATTAATTATA ATCACTTACG 420
 TGTAAACACC AGAACATATA CCTCTT 446

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

CAnAAnTGCT ACTGAAAATT ATTTTITAGA GATAGCTCAA TCACCATAAT TAACTCCACT 60
 TTTTCCATGT GATACACACA CACACACACA CACATAATGT CTTGAACTGT TTTCAATATC 120

994

ATTCTGGCAA ATCTGTCCTC CCTGCCTCTT TCATACCTGT TATTAATTG TTGCTGACA 180
TATAATATCT CTGGCACTGG ATTGTCCATT GTTTTCTAGC TTTCTAATTT TGAAGTCCGT 240
AAGAAGTTTT TTAGTTGTCT AACTTGGCAT TATCCTAATC TCAAGTGAAC ATAAACTTA 300
ACATGTAATT CTTGCCCCCTT TAAATATCAT CATGTGAAGT TGGAGAAAAT GTAGTAACCT 360
ACAGGGCATC AGTGACTTTT TGAGGGGCTC CTTTCAATTA CTTTCTCTAT CTTCATATCT 420
TAATTGCCCA TGGGATGGTG TCTTCATGAC TCCCT 455

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

CGAGATCATG TTTATACTTC TCTTCATAAT GAATGTTTCC TATAACACAA ATCTATGTGT 60
GTAAGGTGTG GAGGAACAGA AAAAACACTC AAGTAGGAAA GAGGAGATGA TGGAGAAAGC 120
CCCACTCAGG ACTCAGAGCA TGGCTTGCTA CATCAAGGGC AGCAGTTCAC CTCCTCGGTT 180
TTGGAACTG TTTCCAGAAA CAAATGGAGA GTGGTTTAAT CAAAGACGCA TGCATGAATG 240
AGTTTGATGA ATAAATTCAG AACATCAATC TGATAATTCA CAGAAAGAAG TGAAGTCCA 300
TAAATAGTCC TATGTGCAAA TCCCAATATG ATCATAAGCT TGCTGAGAGA GGCCAAAGTC 360
AGATCAGGGA AACTGCTAAG TGATTTGAAT ATTTAGTGGC ATCAGGGAAG AGAGTTTGAT 420
GCGTTATCTC TGTAATCATA ATGATCCGGT AAGGAATAAC ACTCCTG 467

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

CAGGGCTTTA TTTATGGGAA AAAGAGAAGT CTAGAGGCTA AGCTGGGTCC ATACCAAGCA 60
GAGAGCAGGC CAGGAGCCAC ATGGAGCAAG TGTTTTGTAT GAGTAGCCAC AGGTAGCTTA 120
GCATGAGTAG CAAAGTGAAG GTACAGAGCA GGCCAATAGG CCATGTGCCC AaAAGGTGTG 180

995

GGGCAAnAAG AGAnGGGnCC ACCATGTTCC AGGCCTTTTA TCCACTTCCA AAGAGGAGTG	240
GTATGTAGC CTGATGGGCA GTGGGTTTAC AGGTGGGGTC AGGTAGGAAC ATGAGATCAC	300
ACAGGGGCAT GGTGAAGATG TGATCTTCCA GCTCACAAAC TTGATCAGTT TTATCCCATC	360
TGCCTGCCGA CATCAACCTC CCCTCAGAGA GATTCTAGCC CTTAATCCTA AGGGCTGTTG	420
AAnGGTGTAG AATTATCATA TACTCTATAG CTGCTTCCTG	460

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

CAGAATGTTT TATGACTAGG AAGCAAAAAG AAGTCAGAAG GAGCCATATC AAGACTATAT	60
GTTGGATGCC ACATGATTTT CCATCAAAAC TCTTGCAAAA CTGTCCTTGC TTGATGGGAG	120
GAACAATAAG AAGCACAGTT GTGGAGAAGA ATCTGGAGGA GCTAGCGTTG GCTAACCTTC	180
TCAAAAACAC TTTCCAGTA ATCAGATGGT CTCATTGTTT ATCGGTTAGA AAGTCAACAA	240
GCAAAATTCC TTAAACCAAA TATTAAGTGT TGCTGTGGCA TTGACGCTGG CCAGTCCGCC	300
TTTGCTTTGA CTGGCGCACC TCTGCCTCTC GGTAGCTGTT GCTTTCATGT GCTTTGTCTT	360
CAGCATCATC CTGGGAAAGC TGTGCTCATG TGTTCTCACA GTGGTTTGAA GAAATGCTCC	420
AGGACTGGAT CCTGnCTAA GTAGATTGTC TATCAAACT GTACTCTTCT GCG	473

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

TGCATTTTTA ATTCTTAGTA ATATTCAGTA TATTTACCTA TGTAATAATC TTTCATTGTA	60
GCCAGGAGAA TTTTCTTCCT GCCCACTGAA CTCTGATGAA GATGTGAATA ACTGGTTGCA	120
TTTTTATGAG ATGAAGGCTC CTTTGGTCTG TCTACCAGTT TTTGTCTCCA GAGATCCAGT	180
AAGTTTGTGT CTCTTATATT GCCGCAAATA CATTAATAAT GCTTCATTTT TAGGATATTC	240

996

ATTTAGATGT AGGCACCTTT TGTTGTGGTG GTATTTTTC ACAACTAGAG CAGACTCTAC 300
AATCTTCTTG AAAGATAATG GAGCAGTGGC TTACCACTGA ATGAGTTAGG CAATGCAGAT 360
TTTACCTTTG AAAAAGTGGA AGGCAGGAGT GCAGGGCACT GTAGCACAGA GGGTTAAGCT 420
GnCACTCTGG GATGGCCTAA CATCCCCGAn GTnGATAGCC ACCCTGGGTG TGGAGTCCCC 480
AGGCCTAATT CCTGGAAACC TTTAAAAAAT CCCAnGCTTT nCCCTGGCCT nAAATGGCCA 540
TAATGGGGGG AnGGGGTnGG GGGGTnGGAA TGGGGnCCCC CAAGGGGnCnA AnCCTGGGGG 600
GGATTAACCT GGG 613

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

TGnGTAATTG CACTAATAGA ATGACCACCTT TGTGTTTCT GGTTCCTGAC AGAATAGTAC 60
GATAGGTGCT CTTTGGCAA ATAAACACT TGCCACTGAA GAAATATTTG ATGTTAAGCA 120
ATTTTATTAT ATTTTCTAGT GCCTGGTCCA TACTATGCAT ATAACCAGTA CTTAATGCTC 180
AAAAAATATT TTTAAATCAA CAGGTCACCTA ACTCATTTCT AAAGTTACAT AATCTGTAT 240
TTTATAAAA TAGTAACAAG ATAAGTGAT ATTAACAGCA CGATATACTC AAGTTCCTCT 300
TACCTATAAC TGACAACACA CATCCTCAA TCATGTAAC TTAAGATTCA GCTATTGAAT 360
TAGTAGTGAA AACTTTCCAC AAGTGGAAT ATTCTTTTCA ACTTTGTATT TTTTAAACAG 420
TCTGCCATTC CTAAAGCTGC TGGGTTTGCT TGCTCCTCC AGTTGGTAAG AATGGAAACA 480
TCAACGATGT CATGGTGTA ATGAGGAGAT GCACTCTCTA GACTGATGCA GCCTTGCAAG 540
TTAGTGCTTC TGTGTGAAGA GAAAGGCTCT TCTGCCTCTG GGCAGAGACA ACCAAACCCC 600
AGGCTGCATC AGCCAC 617

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

TTTtagttat TGGCCATGG GGTGCAATT TTGTTATTT TTTCAAAAAA CCAGTCCTC	60
GTTTGGCTGA TTTTMTGTA ATTTMTTGT GATTCAATCC TTTTGATTTC TTCTCTGATT	120
TTAATTATTT ACCTGGAAGG GAGATACCAT GATCATGGTA GCTTTTACTG GTAGATTTTT	180
GCCTGCAGCA ATGATTGATG TGGTGCTCCA ATGATAAATT GTATTTCCTT AATTTCCTCT	240
ATATTAATTA GAATGTGTCT GTAAGGAAGA GCTGTGCCTA CTCCACAGTT ATTACTTCAA	300
CCACTTATAT CAGTAAGGAC TCCCTGATAT TAATTTTATT GTTTCATCAC AACCAAATGC	360
TTTGTTACTC ATATTTTGC TCTGATTTT CTCAGTTGGA CCCTCAGGAA CTTTTTTAGA	420
CTTGTTCTTG TGTCTTTTC ACATCTTCTC AACCCCTTTG CCACCACCAC TACCACCAC	480
CTTCCAGGCT T	491

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

nACTGAGCTT TTCTGTTTA TTAGCATATA GTTCTACATA GTGGTTTATT ATGACACTTT	60
GTATTGCAGT GGTGTCAGT GTAATGTTTC TTTGTTCACT AATTTTATTT ATTTTAGTTT	120
TTTCTTTTTT GGTGTGTTAG TCATGCTCAA GTTTTGTTTA TCTTTTCAA ATAATACCTT	180
TTTGCTTGT TGATCTTTG TATTGCATTT TTAGTCAATT TCATTATTT CTTTTCTCAT	240
CATTATTTCT TGCCTCCTGC TCTTCTGGG TTTGGTTGT TCTTGTTTT CCAAGCTTC	300
AAGATGCATC ATTATATCCT AATTGAGAC ATTTCTGTCT CTTTAAATCA TGTAATGCTA	360
TAAACTTCCC TCTACTGTAG CTTTGCTGT ATATCTCAGG TTTTGATATG TTATGTTTTA	420
ATTTTnCACT TATTTCAAA AAGTATATAT TCATTTnAAA TTTCTTCAAT GACCTGTTGA	480
TCATTTGGTA G	491

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

TGAGTCCCCA TGACTCTGCT TCATGTTTCT TTGGTACTAC ACTTTCAGAA CTGTACTGGC	60
AAATGACTTT GGGGACAGTC TGTTCTTGCT CTGTTGCTGC TCTGAGCCTT CAATCAAGGT	120
CCACACAAGG CCAATGATAG AAATGTTGCA TCCAGAACAG CCCCCTTATT ACTAAGATGA	180
CCTCCAGGCC CCATAAATGG ATCTTGGATC AGAGGTCAAG ACTTCTGTG CAACTTGAAC	240
ATTTCTGCC TTGGGAAGTT CACTGCnCCC AnCCCCAGGA CATGTTCTGA GCTGCTTGGT	300
CCTAGGTGTA nAGGCTCTGG CCGCTGGGAA TGTTGTACTG AGTTGACTTC TGAGTGTCCA	360
GATGCCAGAA AA	372

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

AGATAGTATT CAAGCTTCAG GTAGGTGGGT TTCAAGCTAT ACACAAAAT AAAGGAGTAT	60
AAAAGTCCTT CATTTGAGGA AAAAAGGGCC TGCTTCACCA ATTTTTTGTA GTACAGGTTA	120
GGCAAGATTC CTTTTTAAAT TTCAAATGTA TGACAAATTC TGAGTTATTC CCTAATGTCA	180
CCTTATAAAT GGATATAGAC CATTACCTGA ACATTGTTTT CTGTGCTTG GTGAGGCTGT	240
CTTACATGAG GCAATGAAGG CTGAGTTCCT AATTTCTTAA TCCCAAAAAn nCTTCTTnGC	300
nGCAAGCATA ACACCAAACCT CGAAGAGTGG TAAGGTTTAC AGTTAGATAn TGCTTGTCTC	360
CTGCATAATT CCACAGGAGA GAGAGTAG	388

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

TTTTCTGAAA TTTAGACCTA AATAATGATA ACCAGAAAAA AACTTTGACA CCTAAAAGGA	60
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999

TTTTGTAGAT AAACATACTT TTAAAACTTC ATTATTGATG AAACATTAAG CTTCAAACCTT	120
TGGAAGGACT TGCAACTTAA TGGTGCTTTT GCACACTTTT TAATAAATTG CTTTGGTATT	180
TTATGCTTTT ATTAGAGGTC GTTTAACTTT TGGTTAAATC GATTGTAGAA AGTCATTGAC	240
ACATATAATC AAAACTTAAC TGTTAAGAGT TAACACATGT AATCAAAACA ACTGCAGATT	300
AATTGTAATG CTGTTACAAA TTTACGTGTT GTAAAATGTC TTATTTTCCT TCTTGTATAA	360
TTATTTATAG AATAGATGTT CATATGTTGG CTGTGGTGAA TCGCAAGTAG ATCACAGCAC	420
CATACATTCT CAGGTGTGTA TATATGAATT TTCAATGCAG ACATTTTTTA AATGTTTCAT	480
TTTGAGATAA TTGTAAAATG GAAGATGTGT TTTTAAAGGG AGACTGAAGG AAAAGGACAG	540
CCAATAATAC AACACTGTTA ATT	563

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

AGGATGGCTG AAGCCCACTT GTCCATCATA CCAACCAGGA ACTTGGACAC AAGCTGATGT	60
AACCAGACCA GAAGACCAAC CATTGTGACT CCAAGCAGTC CTTTATCACC CCACCAGAGG	120
CAAACATATA GCTGTCTATC CTTTCCCCTT TCTTCCTGAC TTCCCCCTTC TTTATAGCCT	180
CTTTAAAACT CCCCAAATAC CCTCATCCAG GAGGGTGGTA ATTCCTAAGA CTTTGGTCTG	240
CTACCCCTTC ATCTGGACAA CAGATTAAAA ATTTTCTTTC CACAACCCTC AATCCTCCTC	300
CTGGTTAATT TAATTTGGCC ACAAGGGACn GGGACCAAGC TTTGGGGnAA ATCGGAnACC	360
ACTGGTATCT GGACATTCTAT CCGATTTTCG TGAGGAGTTG CTGCCGAGTT TGGCTTGAAA	420
ACCAGACTCT CAGAGTC	437

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

1000

AAnAACCGCG TTATTTTCCC TGTTTCTCAG AAGGGGAAGC CGAGGCACAG AGGGGCGGAA 60
 CCTTGCCCAG AATGGTAGAG TGGGATTCAA AGTAAGGCAG CGCGGCTCCA GAGCCCCGCC 120
 CTAAACCACC ACCCAGACGG CCAAACCTGCA GACTGACTCG TGCATTGAGA ACTGGCTCAG 180
 AAATCCCTTT GTTGGGnGGT AGGGGGGGCA GGAAGGCC CACACGCTCT CTGGGACTTT 240
 CTATATGGCA AGTGGAnCGG CTGGCCCTGC TTTCTCAGGC AGAGCTGAGC ATTCTGGAAC 300
 TCTTGCAATG GGCTGGACTC CAGGAAGGCC TGTGTCCCTG CTAAAnCTCCC AGCAGGGTCA 360
 GAGCGCACAA CGCTGTGTGT TCCTAGGAnC G 391

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

ACnCCCATTc AATAnGATGc TGGGCCATGG GTTTTTTCATA AATTGCCTTG ATTGTGTTGA 60
 GGAATGTTC TTCTACACGC AATTGCTTA GAGTTTTTCAT CATGAACGGG TGTGTATTT 120
 TATCAGATGT TTTCTCTGCA TCTATTGAGA TAATACTATG GTTTTTCTTC TGCAGTCTGT 180
 TAATGTGGTG TATCACATTG ATTGATCTGT GAACGTTGAA TCATCCCTGC ATACCAGGGA 240
 TAAATCCCAC TTGGTCTGGG TGGATGATCT TTCTGATGTG TTGTTGAATT CTGTTGGCCT 300
 TATTTTATTG GGGATTTTGG TATCTATGTT CATCAGGAAA ATTGGTCTGT AATTCTCTTT 360
 CTCTGTGCA TCTTTTTCAG GTTTAGGAAT TAAGGTGATG CTGGCTTCAT TGAAAGAATT 420
 TGGGAGGATT CCATCTnTn CAATTGTTTT GAATAATTG AGTAGAATTA AGTTCTTCTT 480
 TAAATGCCTC ATAGAATTCA GCAGTGAATC CATCTGGTCC TGGACTTTTC TTTGTTGGGA 540
 GGGCCTTTAT nACTGATTCA AATTCTGTcn CAGTTTTGGT CTCTT 585

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

1001

GCGGGCGTGG nGAACCACTG GCGCCCTGAC CTGCGGTAC nAAGGAGGGC GAGGGCCACG 60
 GACGAGGCGC GGAGGAGCCG CGGAGGGAGC GGGGAGCCCA GTCCCGCGG CACAGAGCGC 120
 AACCTGAGAG CCTGGGCCAG GGAAGGGGG TTCATGAGGG GAGAAGAGGG CACAGCCTGG 180
 AGCTGGGCTC ACAGACCTGC GCAnGCGAGT CCCCCTGCGA CCACGGCGCC CCGGTCCCGC 240
 GCCACGTGCA AGGTGAAGGG AGCCAGGTGC GAGGCCGCGG GGACTCACGG CCCCCTTCT 300
 CCTAAGTCTG ACAGCAGCTT GGTGGACGCA GCACAGCGGT CAGGGACGCG TGGGACACCC 360
 GCCGAGATCC TGGGGGAnCC AGCGnTCCC TCTCCG 396

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

CCCTCCCTGC CGCCTCGCAG CGAGCTGGGG TGGGAGGCTG AGCAGACGGG ACCCGGCCC 60
 AGCTCTGGCA CAGGAGGTAG GCATCCCAAG CGGTGCTTTC GCCACGCCGG ACGCCTGCCC 120
 ACCCCACAGG TGCCTTATT CAAGCCGGCC AGTTCTCTCG CCCGCGGTCT GGCTTCCCCT 180
 CTCCAGTCCC AGGAGnCCGC GCAGGGnCCT GCTCCCGACC CAGAACCTGT CTTAGGTGCT 240
 AAGGGGCCCC GGGG 254

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

CCTCTGAGAC AGGAGAGGCG GACTGGGGTG GGATGGGGGA GGGCCCCCTG GTGTACCCTG 60
 GGGCCACTGC TGGAGAAATC AGCCAGGGC TTCTCCCCAG GGCAGATCTG ACCCGGACAG 120
 ACCTGAGGGC TCAGCAGGGA CAGCTGCACA CTCACCGCAG GCATAGCCCC ACCCCACCAC 180
 CACCATACAG ACCTGGCAGG ACCCCAGACA CGCCTGCCTT TGTCCCACAA ACATCTGAGT 240
 GCCACGCTCT GTGCCGTGCT GGCTACAAGA GTGGCGGGGA CCTGAGGCTT CTCTGAGGAC 300

1002

CCCTGCGAGT GGACGGAGGC GCGGTCAGTT CCTGGGGGAA CCACTGCAGG TCGGCAGAG	360
CCTGGCCTCA TCCAGGGCTC GTCCAGGGCT CAGGGAGCTG TCCGCACGAC GGAGGCAGTT	420
TCGTTCTGTA CCACCGGCAG GCAAGAGGTT CAGGGCGGAA CCAAATCAG CTCCACCCGC	480
AGCAGACAGA CGGCGTCGCT GGGGCGGAAC ATCAGAGAnG GGCCGCGGAA GGCGGGGGCT	540
CTGGCTGAnG CA	552

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

AGCAAAATAC TTAAGAACTG AAATGAGCAA AAAGCAGTTT TAAGAATATA GGTCAGGACA	60
TTAATAAAAA TTTGATCGCC TCCTTTTAT TCTCTAACAT TCCCCACAAT AAATCAGCCC	120
AGTTTCCCC AGCCCTCCT CACACACACT TCACCTCCC GTCCTGATTT CGGATCGCAG	180
AATGTAAATC TGTGACAAGG GTATCTATAT ATAATATTAA TGGTGCCGAG GAGGGCTGGT	240
GTGAAGTGTG AGAGCTTGCC AAGAAAGGAG CGATCTGAGC CCAGCCGTC ATCCTGCGCA	300
GTGTGCTCTA CATCATCCAC AGGACAAATG TAACATCATT AGGGGAAAA AAAGGAAGAA	360
AGAAAGGGGG CAGGAGGAGG TAGGGAAGTA GCCATTCTGC AAGGAAATGG CCAAGTTGGA	420
G	421

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

GGACTTACTA GATGTGATCA GGATAAAGCT GGATCCATGT CACCCAACAG TAAAAAACTG	60
GAGGAATTTT GCAAGCAAAT GGGGCATGCC CTATGATGAA TTGTGTTTCC TGGAACAGAG	120
GCCACAGAGC CCCACCTTGG AGTTCTTGCT CCGGAATAGT CAGAGGACGG TGGGCCAGCT	180
GATGGAGCTC TGCAGGCTCT ACCACAGGGC CGACGTGGAG AAGGTTCTGC GCAGTGGGTA	240

1003

GAAGAGGAAT GGCCCAAGCG GGAGCGTnGG AGACTACTCC AGGCACTTCT AGATCCCTCT 300
TCTTCCTTCA TTGGCCTCTC TGGACTTTGA AACCAACCACA AGTCAAAGAG GAATGTGAAT 360
CTGTCCTTTT GGAGTGTAGA ATAATGATAT GAAACTGTGG ACATTAGTTT TCCCCAAAGC 420
TGGTGATTTT GTGGAGGGGT AGATTGTGTT TGGTGGTGA TATTGTTTCT TGGTTTTTGC 480
ACATCTGTTT TAATTTAATA TTGAATCTGG AGTTGGGAAA G 521

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

AGGCACCATT TCATCCCAGA GTCCAAGCTG AGAGCAAAAC GGCCTGAACT GCACCCCGGG 60
GACAGTTCTC ACTCAAGAAA ACACATTTTC CTCTCCCAAC CTAAATTTGG AAGGAATATA 120
CTAGGGTTTC TCTAAGCAAA CAACTTGTA AAACCATCGG GGGAGGTGAG GCCGCAGGCC 180
CGCTCTACCA GGAGCGCCAT ACCAGCTGCC TCTGGGACCA CCCCATCCTT CAGCTCCCAA 240
GGGGCTGCTT AAAGACTCAA CGTCTCATTC TTCATAAACC CACCTCCTAG TCATAAGCCT 300
CAGGGGAGAC TTTTTTTTAA GCTGGTAGTG ATTCTTGGGC ATAATAATAT ATGACAAAAA 360
TGAGGGCATG GAGGAGTTAG ATAGAGCTCA GGCCAGGTGA AGGTCCTTGC ATTCATCTCC 420
TGCAGCTGTG GCAAAGGAGC AAAGGAAACC AAGCCAGCAA GAGTGTGTTCC GCTGAGCAGA 480
AAAGGAACGG CTCTGACCGG CATGCAAACA CGCCTGCTGA GACCTCCTGC GT 532

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

TTGTGGCCA ATATAGTTCA GAGGGGTCTG TGTAGGGGAA TTTCTGATCC CGACAGGAAA 60
TTCTAGGTCT GTGGCAAAAA GGTACTACC ACTTTTGTA CTCCCAAATC AACTGAAGCC 120
TACCTGGCCA TCATAAACCT TCCCTAAAGG GCACGGCATT CTTGACTAAT CAAGGGAAGG 180

1004

TCACAAGCAC CACTATCAAC CAATAATTTG CACATGAGCT GGACATGAAC TTCTCAGACT	240
CAACTTCAAT CTGTTAAAAC CTTCACCCCT GGAGAGTCTG GGAATTAATC AATAGCTGCA	300
CGGCCTCTTA TTCTGTGCTT TGCAATAAAT GCCTACTCTC TTCCACCATC CGATGCTAGC	360
AATGGCTTCT CAGTTGGGCA ACCAGACCTA GTTTGGGGTT CTATAGAAAG TTCTCCAATG	420
AGTTTGGGGT GTCATTGGCA AACAAGTACT CCAAGGAGCT GACATCTCAT CCACTGGAAC	480
TGAGGGCTCA TGGCATATCA CCAGACCAAG TAAATGAAA ACGGGGACAG TT	532

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

CAACAAATGC AAATCAATAA AGGCAATACA CCACACCACA TCCACAGAAT AAAGAATAAA	60
AATCACAAGA CCATCTCAAT AGAGGCAGGA AAGGCATTTT ATAAAAATCT AACATCCTAT	120
CATGATTAAA ACTCTTAACA ATTTAAGAAT AGAAAGATAA TACCTCAACA CAATAAAGTT	180
TATATATAAA AAACCAGCAG CTAACATCAT ACTGAATGGA GAAAATCTGA AAGCTTTTTA	240
AGATAGGTCA AAAGACAAGA TTCAACATAG TACTGGAAGT CCTAACTAGA ACAGTTAGAC	300
AAGAGAAGGA AACAAGGTCA TCCAAATTGG AAAGGAGGAA ATTAAATTGT CAATGTTTAG	360
GCTGACATGA TCTTATACAA GGAAGAGTCT GGAAACTGT TAGAACTAAT AGATTCAGCA	420
AAGTTGCAGG AC	432

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

TTGGAAGTnA GAGCGnGAGA ACCTGATGTT GGACATGAAT TTTATTTTGC TAATGATCTT	60
CACTCAACTC TCTGAAGGTA TTTTACCATT ATCTTACTAT TGTTAATTCT ACAGTCCTTT	120
ATAAATCCAC ATAAATGACT TTTTCTATT TGGCTGCTTT TAAAATCTAT TTATCTTTGT	180

1005

TCTTGCCAAG ACCCTGTACA TCTAAGTACA ATTTTCTCTC TGCTGTCCTA CTTGGGACAG 240
TATGCAACTG TGGATTTATG TTTTTCATTA GTGCTCAAAA AACAGCAGCC ATTTCTCTTT 300
CTTAAAAGAT TATTCATTCA TTCGAAAGGC AAAATGAGAG AGACCAAGAG AGAGAGATGA 360
GAGACAGAAA GAGAGAGATT ATCTCCATCT ACTGGTTCAC TCCCAAGACG GCCACAAGAT 420
GAAGCAAGGC CCCAAAACT CCAACTGGGT 450

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

TGAATTAGTT GGACAAAGCA AAACAGAAAA ATTCTGGTGG TAATAAGTGA TAAGTCCACT 60
AAGAAAATAA GCAGAGCATA GGTAGGGATG TCTGTGTTAG GGCTGTCAGG GTCTATCCTG 120
CCTCTCTAGG CACTCAAATG TCCGCTAAAT ATGTCTGAGT TGGTTTGTTT ATATTATGAT 180
AGAACCTTAT GCTTATCTCT CCTACATACA CATGTAGATA CGAGAATTAT TTATGTGATA 240
GTTCAACCCAG TTTTATGATT CAGAAGGTGA CACCTCAGTC TTCCATGTTC ATAATTATTA 300
AAGACTATAT GCCTTAAACA ACCTCAACCT TCCACTGCAG AACAGCACAT GTTTGTGGCA 360
TTGATGATTT TTCAAAAAGC AGAGGCCCTT TCTTCAGAAA AAGAGAAGAG GCAAATAGAG 420
CTTCATGAAC TAGATTTAAA ATAGGGGCCC ATGCTGATAG CCACTGTCAT CATACTGTGC 480
CTTTTGGCCA CCAGTCAGAT GCAGGCTCTG AGCTTAGATT CCCTGATTCT AGACTCTGGG 540
GGGACCTCTA AGCCACTGTC AGAATTAGAA ACCAAACCTG ACTGAATGCC CAGAGATTAT 600
CCTTAATCTG CTATT 615

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

AGTAAGTTTC AAAATTATGC CAACATGCAG GTCCGTGATT GTCTTGTTTC CCTAAAGAAT 60

1006

ACTGGAAGGA AGAGGTATTT TTA CTTCCTG TAAATTTATC TCCTCAGGCC AACAGAAGTA 120
GACCCCTAAA TTCCAAACAG CCCACCCAGA TCACTATTGC TAGAGAATCA CTGGTGAGGT 180
ACTTGTGTCT CCCACCCCAT TTATTTCAAG TAGCAACAGG ATGATTTTTT AAAGAATTTT 240
GCTGGCCTTC TTTCCTAACT GCTTTTTTGG CCTTCTCCTG TCCACTTCCT TTTTATTATC 300
CTGCAAAATG ATTATAAACC CACAGAATGT TTTAGACTGG TGAGTGCCTG GAAGGCAGAG 360
CCAGTTCAGT AGCCATCCCG GTGAGCCCAG ATGGCCCAAC AGGAACGTGT GCTGGAAATG 420
GGCCCAGTT 429

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

TTTCCTTCGA CGATGTCATC AGCGTGCGCT TTGCCTGAAA CACCTCCGTC AATGCCTTGT 60
ACATCATCGA GAATCTGAAA TCCTATCCCA ATAGGCATGA CTTGCGCTCC AAAGGACnGG 120
CCTCACGCGC AGAATAACCT GCACACAAAA ACCCCAATTC GCCTGATAGA GCGATGAGTG 180
CGCCAGTTTT CAGTGCAACC ATACGCAGAT ACTGCGCACG CGAGGGAATA AGTTCTGGGC 240
TGCGATGCCA TGCAATATCA AGCGCCTGAC CCATATGAAG AGCACGCGTT GCACTTATCG 300
TGGCAGAAAA AAGAGCCGCC TTAAGGGCAG GTTCTATGCT GAGCGTGTCA ATGAGTGCCT 360
GTGGCATGAA AATACAACCA GCTTGCTGGC ATTAAGAACG CAGTCAGTAC CGTAGCGGCA 420
GATACGGCAC AT 432

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

ACGGGACTTA AGGAATGTGA AGTGATCCTA GTTTAGACCA GTCTTGTA CTAGCCTCGCC 60
GTTAAGACAG TTCAGGTGCC CACGGCCCAC ACTGGAGTAC CTGTATTTGA CTCAGCTCCA 120

1007

GCCCCCTGGCT CCAGCTTCCC GCTAATGCGC ACCTTGGGAG GCAGCAGTGA CAGCTCAAGC	180
AGCTGTGTCC TTGTACCCCA GGC GGAGAT CCAGACTGAG CTCCCCGCTC CCAGCTTCAG	240
CCCGAGTGAG GGCTGTTGTG GGCATTTGGG GAGGAAGCCA GACGATTGGA GGACACTCAC	300
TTGCCTTCCA CCCTTTCTCC CCCTTCTATT TCTGATTCCC AAGTAGGTAA AATTTAAAAT	360
AAATACATAA AATACTCCCC AGAACTAGCT CCTATTTTAA GTCCAATTAT TACAATGTCA	420
CAGATACTTA TCAACAGGTT AGTCATTCTT TTCCATTTTA ATAGGAAATG AAAAGGAAAC	480
TAGGGCAGAA AAAATTGGTT TTAAGATAT AGTGATGGGG GAAGAATGAG TTTTCTCTGC	540
TCTGCTCTTC TGAGTACTGA GGTTCATGGG GGACTTCCAC ACAGGAGCTG TGTCTCTGGG	600
TTCACCTCTC CCCCAGAACA CGAGTGACnT TAAACTGG	638

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

GAATCCCGGG AGACTACAGT GAGGACAAGA GTGACAGTTC CTCCCCCATG GGCCACCAAT	60
CTGGTGGAGA GGACAAGAAA TGAACAAATA GGGGGCAGCA TTGTGACCTA ATGGGTAAAG	120
TCACTGCCTG CAGCGCTGGC ATCCCAAATG GGCACAGCTG CTCCACTTCT GATACAGCTC	180
CCTGCTAATG CTCCTGCGAA GGCAGCAAAA GGCGGCCCAT GGGAAATGAA CAAATAATCA	240
TTACAAAGCA TGGCATGTGC TTTCAAGGAT TCTGCGAAAG ATGAAAGTTG GGGTGGGGGT	300
GCTGGTGGCC AGGTGAGCGG CCAAGGAAGA AGCCGGATCA TTTGCTGGCA CCTGGCCACT	360
GACCTCCTGG GCCAGGCACT ATGTCACACA CACCCAGGGA GAAGGGAGGG GAAGGTGACA	420
TCCAAGGACT GAGGCAGAGG GAGAAAGGGG ACAACTCCAC TGAGAGGAAC GGGGCATTGT	480
ATGCTAACAC AGTATTTGTG AAGCCGAGGG AGTGGAGGGG GCTCTGATAA CTCTCTAAAC	540
AAAAGAGCTT GTCCTGGGCA CGGGGAAGCC TCTTCAGTGC CTGCAGGAGC CAGCTCTAAC	600
CACCTGGAAA TCAGTCATGG GGTGACAGCT GAGCCCAGGA G	641

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

ACATCAAGTG ACAGCAGATA AAGCACTTGA CTTTGCCTCT TAAACACACA TTCCTGGGAT	60
GAAAAGAGGC TTAGAAAAGC AGGGCTGGGT CTGTCTGTTT TGTCAGTGTG TTTACCGTGT	120
GGTCTGCATT CATCAGGGTC TCCCAGTGCA GTGTTTGGGG TCCTGGCCCA GAGAGCAGGA	180
CCAGGAAGTG GCTGGGAGTA CACGAGGGGG TGCATGTGCG CGCCCTCATC CAGACGGCAT	240
GAGGTCCACT TGGCTCCTTC CTATCACGAC TCTTCTGGAA GTTCCAGAGG ACGGGGTGGG	300
GGGAGCCGTG GGGGGCTGGG CAGAATAnTG TGCCTCTGGA CAGGAGCACA CAGCAGTTTT	360
CAGGGGGCAA nTGGGAAAGC AAAGTCAATT CTCTGACCCT GAGGGACTAG CCTCAGTAGC	420
CTCCTATCTT TCCTCCTGAA AAGTTGChAT TCCACCGTG AGCCTTTCAh CTGTCTTATT	480
TTTCAAAAAA GATTTATTTA TTCACTTTGA AAGTCACACT TGAGGAGAGA CAGAGACATC	540
TTTTTGCTGC nTCA	554

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

ACCCTGCGTC GAAATCAGGA ACCGTCTTGA GCACGCTTGC GCAGGACTTC AACGCTGTAA	60
ACACCTGGAT ACCGCCGACC GTGTTCAATCA GATTACTCTC ATCAAAACGC ACCGTAAGCG	120
CGTAGACAGA GTGCTCAGGC GGAACGATCT CGCGCAATTC CAACCGATCG TATTCAGAAA	180
GAAGAGACAG CGGCGGCACT CGCCCTACCT GAGGGGCTTC CGTCCCATCT TCACCTACCG	240
CGGTCCCCTT TGCAGCTTCG GCTGCATTTG GCGAAGACAC CGACAATCCA CGCGCCGCCC	300
CCGGCACAGT CCCAGACGCA GGCAGATACG AGCGCAGACG CGCAACGAGA TCCGAGACAT	360
CCTCCGCGTA GGACCACCGC CCGCACGGGA CTCGAGCATC GCCTTAATTA CATCCAACGA	420
CGTCAGGAGC AAGTCCACAA CCGCCCCGTC AACAGTTACC TTCTCTGAGC GAATCCCATC	480
CAGCAGATCC TCCACCGCAT GCGTGAAGCC GGACAACTCG TGCATCTCAA CAGTCGCAGC	540
ACCCCCCTTA AGGGTGTGCG CCGCAGGAAA ATCTCGTCTA CAGC	584

1009

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

AAGTACATTG AATGAAACTT CAGTGACTGC CCAAATGAAA ATAAATCCGC AGTCAGCCCA	60
CCTCCCCACC AAAAAGGAAA AAAAAACAG GAACCCCGCT GCGATCTTAA CATAACAAA	120
CAAAACCTCA GAACCGGTTT TTCAAGCTTC CCAGTCCTAC CnnnnCACCn GCnCCCCCA	180
TCCCCATAGG TTCATACACC AGCTGCCAGT CCAGTCTTTA AGGATAAnAn ACCACTACAA	240
TGTAGCACTT TCACTTTCAT TTGCTGGGAG AAAGCCACTG GCGTTAAACT GTGGAGAATA	300
TGCCCAATAT GTTTTCCATG TCCTGAGCAA GCAAACAAAG TCTGGCACAC AAATCGGAAA	360
CAGGGAAAAA TGTGAAAATA GCTCAGGACA AATGCTGCCT TTCAGTGGTG TAATCTGCTG	420
CATCATTTAT CTGTCTCTAC CGCTGAGTGT AGGGTTTAAA AGTTTCTGAG ACTGGGGGAG	480
GGGAAAATTG ACGCCTTGAA AGTCCAGTCC TAGGTTAACG CCAAGTCAAT TTCCGATGGC	540
CACAACCAAA AAGCGGAATT GGACTTGAAG GAAGGGGG	578

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

GnAGTTATTA ATGTTTAAAT AGTAATAGTG GTATGGTAGT TTTTTTTGTC CTTTATTTT	60
ATTTTTTTAA GGGAAAGAGT TTATTGGGGG AAACCTGACA GACTGGAGGG AAGGGGCAAA	120
AAAGGAAAGA GGGAGAAGGA GAGCAAAAGA GAGAGAGAGA GAGAGACAGA GTGTTCAGGA	180
GACGGAGACA AAGAGAGTGT CCTTATATTT TAGAAATGCA GAGAAATAAT GAATGCAATA	240
AAATGATGTC TGAGATGGGC TTTAAAATAA TCTCATGAAG TAGAACAAAT CATAGAAATA	300
TAGATGCAAC AAAATCCACC AATCTTTGGC ACTTGGTAAA ACTAAATGAT AGCTACATTG	360
GAGTTCATTA TACCATTTTT TTCCTTTTGT CTATGTTTTA AATTTTCTGT AATATTAAAA	420

1010

CATTTACATA TGTATAAGTA TGAAGTTAAA TCAACATTTT ATTTCCTCATT CTCATAATTT 480
 TTTACTCTTA CTCATAATGT TCTTAATTGT TAGGAAGAGA CAAGGAATTT GTTGGGAATT 540
 TPTCATTACT CTGTTTAGAC GCAGGATGGC ACTCTTTGAA TAAGTAATTA GCTAAAGTGA 600
 GTAAGTnCCT CTACAGTTC 619

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

AGGACAGGAT GACAGCATTT CTCCTGCGAT GCAGAAGCCA AAAGTGACTT AAGGAACTGT 60
 CCTTAAACAC AGACATAAGC ACAAAGACAG ATGGTGTCAC TTTCTTAATC TGCACAACTA 120
 CACATAACAA CAGAAATAAA CTCTTTCACT CTGTATTGGA GCCTTGGGTA AAGCAACCTC 180
 CTCTTAACCT TAACCAAGAC CTGGGAGAGG CCACTATTAC AGAATGAGTC CCATTGACTC 240
 CGCTCACAGA TCTACAGTAG GAATCCTCTA TTAATGAGAA TGTGGTATGG ACTAGATCAC 300
 ACAGAACTTG TTGCCTTCAA CTTAACCTT CCTCCTGCAA CCCCACAAGC AAGTATTGTT 360
 TCAACTTTTA AACATAAAGA ACCTCATACC CATAAAAATC AGTGTCTCCC TCAAGGTCAC 420
 AGAATTTATT CATAGTGAAC TAAATTTAAT TTTnnnTTTT TTTTTTTTTT TTTTACAAA 480
 TCAAACCAGC AATCCTTATT TTAATTCTGT GGTAAATAAG ATTCAAATAA ATTATAATTC 540
 TCAACTGAAT AGAATTCAT 559

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

CTGnCAAAGA GCTTGTAAGT GAAACTTAAT CTCCAAATTC ATCTGTAAAT GCTATTTGAA 60
 AGTGAGGTCT TTGGGAAATA GGATCACATG AAGTCGGAGA GTAGCACCTC CATGATGATG 120
 TCAGTAGGTT CACAAGATGA GGAAGTGAGA CCAAGTTCG CATGCCTACT CTGTCTCATG 180

1011

TGATGCCTCT GCTGGGCGAT GATAGAAGAA GACTGTCATC AGATGCAACA CCATGCTCTT	240
GGCTACGAAG CCTCCAGAAC TGTGAGCTGA TGAGGCTTCT GTTCTTTGTA AATAACTCAG	300
TCTCTGGTTA TTCTGACAAA AAAGTAAATT TCCAGGCTGA TACTGTGGAA ATCTAACAGA	360
TTTTTCGTCT CTTTCTTGCC CTGCCATTGA GAACACATGG GTCTCATGTT GAGATATAAA	420
AGCTTCAAGA TCCAGGTTAC TTGGCTCACT GCATCTCTGT ATGGAGGCCA CCTGCCACGG	480
AGAGTGGCTT GGACCCACTG CCTAACCTTG CATGTGTTTA GTAAAAATGA TGAGAGTACG	540
AGAGACTGTT TAGTCTACCT GAACACAGGC TGCTCTATCT GACACAGAAT GGATGCAGAA	600
ACTGCCCATG TCCAAGTCC	619

(2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

AACAACACCA AATTCGTGCT GAGGTGGAAT AATCGCTTTG GCTTTGTCTC CCGCTTCAGG	60
CCCAGCTTGT GCAAGTCTGC AGAGGCAGGC CAGAGGGGAG CTGAAATTTG GAACCCATGG	120
ATTAAGCAAA CTACGGTCTG AGGGAAGAGG TTCTTCTAGC AGGGTTTCCC TGGGAAAAAA	180
ATCACCTCAA CCGAGCACCT AAGTCCTGAG TCCTCTAACA GGAGGCAGCG ATAGAAACCA	240
ACTAAACACC CAAGCCCTCC GAGGGGGGGA TGAAGTGGTC ACGAGCATCG CCCCAGCATG	300
CCTGAGGAGA GAGTGACCTC TCTTACCAAT CTGATGGGCT GAGAACTAGG TCCGATGTGG	360
GCATGCAGCG ATGAGATCAG GCAAAGGCTC TGGCTGTGAA TTCGCTCAA ATGAGAAGTG	420
CAAGAGGGAG TGAGAAAATG TTCTGGAGAG GCGTCTCTCA GGGCCTTCCA GGTCAGAAGG	480
GAAAAAGGAG ATTGTAGGAA AGAGAAGGTT AGGGGTGGGT GGAGACACTA AAAAGGGGAA	540
GGATTTGTCC AGATGAAGGG TGGGGGGGTC ACAGCTCTCA CCCAGAGAAT ACGAGATCGG	600
CAGATTGGGA CAAGATGCTG GCCCTTCCCT CTATTTCTCA CACGGGGCAC CAAATATAAG	660
CAAAAGGGTG CAGATCAGAG A	681

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

GGnACAATTA CAGGGGAATG GAGGAAAAAT CAAATTACAT CAAATCCGGT CATTGAGTCA	60
ATTGCTACTT TTCCCCAGGA GGAAATTTTT ATGCCATGAA GTACTAGGGT TGTATAAAAC	120
CTTTCAGAT CACTTTATAA AACTTGTTTT ATACACTTGT ATTTAGTATT TACATAGTGG	180
ATTcAGCAGA AGGTTGATGT TGACAGTGTC AGTCTGAGAG GACTGACCAG GAnTACTTTT	240
AnTGttCAGG GAATAGTAAT ACTTACCCTT ACCCCTTAAC TAATAAGGGG nGGTAATCnT	300
TnTAGTTAGG TTtAAGTTTG AGTACCTCTA CTTGGACGAC ACTGGGCACA CTCCTGCGTT	360
TTtGTATATG TTTTCTTGGG AGTGTTACAG ATTTGACTGA CATCCTGTAT ATATAATACT	420
TTTAAAACAG TTAGTTAAAT GCTTGGTCAT TAATGCCATA AATTATTAGA TATACTCTTA	480
CTCAACTGGA TGTGCAGTGT CAAGGAGCAG TCATTTGTCA TTATTTGGGA CACTGACACC	540
CAGTCTTGGa ATATTGGAAT GCCTATTTGC AAGATC	576

(2) INFORMATION FOR SEQ ID NO: 502:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 681 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

TCAGCCCGGA GTATGCTAGG TTCACACTCT GGGACTATGA TCCTCAAGGA GTGGGCATTC	60
CAGAGTTGAT GATGATGGTG ACAGTAGTGG TGGTGGTGCC AACGGCATTG CTGTGGGTTT	120
GAGGGGAGTC ACTGTGGGAG GAGTAGTGAT GGTGATGAGG TTTTGCCAAG AAAAGGATGT	180
GAATCAGCGA TGCTTTATTC AAGGAGATAT GAATCAAGTC TGGTCGAGAA AGGTCAACCA	240
CGACAGAAAG TCCAGAAATG TTCGTTTCCA AACTCTCCTA AAGTGAAGGT GAAAGCTTAA	300
GAGTGTAATA TGAAGGGGCT TTATTAGATG ACATCTACGG CATTTCTAAA CCTACCCAAA	360
AAACTCATTT TATTTTATAA TACCATGCTG CCTCTTAAAT TATTTTGTGT AATTGTCCTT	420
GTTACCAAAA AAGAATATAA AGACCTTTTA AGTTTCTTTA GTTTTAAGAA TGCAAAATTA	480
TATCAGGCTT GATGGAATG GAAAGTTATA TGCAGATTTA CTACTCGTAG ATTGCATCTG	540
AGTTTTTTTT GTTTTGTTTT GTTTTACAT TTCTATCACC TCTCTGCCAT GTAGTGAATT	600

1013

AACATTCCAC CATTTCAGG GAAAGGGATA ATAAGGGTGA AATGTGGGCT GGAATCCnAC 660
CAnCGTGGTA GGAAAATAAT T 681

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

TGATGGTAAT ATGAGAAATG CTGCAAGGTG GAGCGGGGCT GAATCACAGA AAGTGGAAGC 60
CGGAAAGTAG ACTTATTGAG TTCAGAGAAT GGTGGCGAT CAGGAAGGGT GATCCAGGAA 120
GGCTTCTTGG GGGAGGAAGG GCTTATTGTT GACCAAGGGA GCCCTCTCAC CATTTACAG 180
GGTGCTGTGA GATTCAAGAC AGGTCAGAG AAATTGCACA TCTATGATAA ACTGGTGAGA 240
TGAACAAGAA CCCAGGAAG GCAAAACCTG CAGAGTTGGG GAGGGCGAAG GAGGAGAAAG 300
GATGCTTCCA GGATAGCAGT GCGGACTGGA TTGAAATCAC AAACGCAATC ATTCATGAAC 360
ATTCTATTCC CGGCTTGGAT CAGAGGCACC ACAGAGGCGC TTGGAAAAGT CAGCTGGAAA 420
GAGAGACCAG AGAGAGTCAG CTAGAGAGAC TGGACAGAGG TCAAGTGTC AAGCTGCAAGG 480
TAGAGAGAGC TGGAAGTGGC TGCTGGCTTG CCTGCAATTC CAAATGAGCT ATAAAGTAGA 540
GAAGAATCCC CGGATCTTCT CTATCAGGTC CACAAACGTT AGAGGAnCGG CTATGTGACA 600
AGGTCCTTA CTGGTGGAnA AGAACTTGG 629

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

AGTCTCACCA TGGGTGAACT TCCTGCATGG AAGTTTAAGC TGAGAAACAG AGAAGCAGTG 60
GGCAGCCGGG GTCACAGAAT CCAAACCAGC AGGTACCAA GGAGAGAGAT TGTGAAGGCT 120
GAGTGAGGAG AGGGCCTGGC AACATCACAG CCATGGTCAC ACTCATGGTC ATGGTCATGG 180
TCAGGGTCAG ACTGGTTCCA TTTTACTAAC ACAAGAAGAA ATGAAACATA AGCTCCTGCT 240

1014

TCCTTGGTCA GGAGGCGGCT GCTCATCCGG AGGCCCATAC TGCCTCCCC AGCCACCCTG	300
GCTTCACACC CGTGCCCTCT GTCAATGCTG TCTCTGAGAC AAGCCTTCTT CATGGCATCC	360
CTGCAGCCCA TGCTGTCCCC AGGGCCGCCT CAAGACGTAG CCTTCAGCCT GACCTTCCTC	420
CACGCCTCCA GCTACCTCCT GGAAACACTT GGTGCTTCTC GATGTAGATC TGGGGCTGCT	480
GCCAGGCTTA GGCCACCTCC TCGTCCTGGT CATGGACTTG GGGCTTTGAT GTCACAGTTA	540
AGGTTAAGCC CAGCCGCTGC CACACATACT TT	572

(2) INFORMATION FOR SEQ ID NO: 505:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 626 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

AGGGTTACTG TTTTAGGTTA ATGCCCTGTG ATTTTATGC CCCTTTATGC AAACAGGAAT	60
AGTGTCTGTC TTTGAGATC TAGAAGAATT GGTTCCTGG CTAGAAACAA GTTGAGGGAT	120
CGGTAAAGGA ATGGGGTGAT CTTTCAGATG CCCTTTCCAC ACTGAGAGGA GATTTTGGGT	180
TCCTGAGCAG TGAAATCTCA AATACAGCTT TAATGGGTGT CCATTTGTAT GTAACACAGA	240
AGAGAGCTGG CCTTGAAAGA GAGTCATTTT CTTTCAACAT TTCTGAGAGA AAATCAACAA	300
CCTCAATTTG GCCCAACAAT CATTTATGCT GCTTTTAATA TATAACAGAC TTAAAGACCA	360
GCACTGGGGG TATTCTGATG AATAAACCAC ATTCTCTACT TTAAAGGATA GCCTAGCAGG	420
GGCTAAGTTA TTCATTTAAA TAATTTATGT CTTTCATGAAA CTGGGAACAT ACAGGGAGAA	480
ATTGCTGGTG GATTAACAGG AATTGACAG GTCAGGATCT GGTTATCAAT CACACTCAGG	540
AAAAAGGCAA AAGCAAAGGA TGAGGTGAC CTCAGTGCCA AGGTCATTGG ATAGTGAGGG	600
TCATTGGCCC TTAAGCCATA AAAGTG	626

(2) INFORMATION FOR SEQ ID NO: 506:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 583 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

1015

CAGTGCCTGn TAAAGAACAC TAAAGGGTAC CAAAGCTAAA TGCAGCAGAA TTGAAGTTTA 60
GCAGATGGAA GGGCATCTGA GCCTACACAG AACGAGCTGT CCACAAGGTA TAAGGGTCAG 120
CCGTACAAAA TACCTTGTGA GGCTACTACT GCAAGCATGC AACCTTCCCA GGAGAGCCCC 180
TCTGAAGTCG GGGCTCCATT ATCTCAACTC TCAAGATCCA AATCTGGGGC TACATGTCTG 240
ACAACCACAC TGGCCCTTC AGAGAGCCAG TTATGGCCTC CAGGGAAGTG GTGTTAAGGA 300
CCTTCAAATA AGAGCCTTAG GATCTCCAGA ACTACCAAAA CCTACACTTG TAGCAGTTGG 360
GAAATTTAAG AGGTTAAGCA TTTCTCCTAT CAGCAATTAA AATGTTTACA GAGCAAGGnA 420
AACTCTTAAA CCTGAATGAG CCATAAGCAG ATACAGATCG CCACAAATCT ACACCATTC 480
TGTGACACAA GTCTATACTC CTAAGCCCTC AGAGCAGCCT CTCTTTCTAG AATATGCAGT 540
CAATnACACA AAGTGnCTTT CAATGCTCTT CCACTCATGC TGG 583

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

AGAAAACATC AAAGATATGC AACTAATGGC ACTGAAGAGT TAAGAAGAAA GTGAAAAATT 60
ATGTGTCCAG GATCTGAGAA AAGTACAAAG AGGATTATGA AGACGAACCC TTGCAGACAG 120
AAGTGGCATT TGAACTGCT TTCTTCCTGG GAATATCTGC CAGTTCAGCA AAGAACGGCT 180
GACAGGCTGA GAGGTGCAGC TGACAGGGCC TTGGCAGGTG GAAACTGGAG TCAAAAGCCC 240
GCCAAGGGAG TTGAGCTGGA AGGAAAGCGA AAGGGAnAAT CCCTCTCAGG AGCTCAATCT 300
GTATCAGGTT GAAACCCTAA GGGTACACCT GAAATGGACA GCCTTCAACA TGCTGnAGCC 360
CAGCCATAAA CTTCATAACC CGGGCAATCA CACTGAGATG ACTTGAGCTT GCTGATGCAC 420
CCAGCAGAAG TGAAGACATA TCTTGATTG GnAAAGATCT CAAGTTAAGA ATATAATAAC 480
CCTTCTAATA AAAAGTCCAG CACAGAAGGA GACAAAAAAT GGAACCAAAA CCCATGAGnA 540
ACAACAGACA AAAGAGACAG ACCCAAAAGG GCTCCAACAA TGGTnAATAT CAGGGAACAG 600
ACCTTTG 607

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs

1016

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

TGGCTCAGCT GGACTGCCAA GGACTCCTTG AGCAGCTCAG CTCAGGGCTC AGCCGGGCCA	60
GAATCAGACA TTCAGGTGCC CCTCCCCCG CAAAGTGCTT GGTGTACCCA CGCAGAGGTT	120
ACAATGGAAA TAACCCCGAT CCATGTAGCT TCATATTTAC ATGCACGAGA AGAGAAAATG	180
GCCTCTTTTT TAAGGACATT CATCACAGCA GAATCACCTT CTGCCGCTTC GCTGTGTTAT	240
TGCTGCTGCT GCCTTGCTGC CGGCCCAAGC TGGACTCAGT CTGCCCGCTG GCTCACTCAG	300
CGCAGGTCGG CAGGATTTGC CCGACCGGCT TTGGGATAAT GAGCAGCCAG GCTGTTGGTG	360
AGCAGTCCCA CAGGTGCAAG AGGCCAGTAG CCTGGTGGGC AGCTTGCTGA GGCCACACCA	420
GGTTTGGCAG GTGCTCAGGG TGAGGACTCT GGGGAACCTT CCCTGGGG	468

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

GTCACCAGAT CTACTATATA CGTATTTCTT TCCTTCCCCA TTCTTGGTCT GCTCCATCAG	60
CATTTTAACT CCATGGGGGC AGAAGCTGTC TGTTCATCG ACACCAGCAT CCTCTGCTCA	120
AACTATGCCA GTATAATTTG TTGAATGAAT GAAGCCAATA TATTTTCTCA AGTATAGAAT	180
CATTAGATT AAGATAAGGA AATCTTATTT AATATGGAGG TAGAAATCTG GATGAGGCTT	240
TCGTTTACA AAATTATCTC TAACTTAGAT CCATAAGTGG TGTCTGACAT CCCAAGTCAG	300
GAAGCATTCT GTTTAAGGAA ATCCACCCAC ACAGGGCGCC AAGAAGCCTG GGGCGGGAGA	360
GGGAAGTAGA CTTGCCGTAA AAAGCTGTAC AATGTAAGCA GTAACCTACCA TGCCCCGAAG	420
CCTCAAGTCC CTCAGCTACA AGATGAGCAT CATTACTAAC TCCTGCCCTC CTCTGGGACA	480
GTTTCTnTCG TCATCAAGGG ATCACAAATG TAAGCCCCCC TCCTTTTTTT TT	532

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs

1017

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

GGGTACGCGT CACAGCATTT TATTTTGTGA AAATGCTCTG CTTAAGGGAT CTAGAGCCCT	60
AAAATTACCA AAAACGTTCA TTGCAAACGT CTCGGGGTGC CTTAAAAGTG CTTCAAGTTCG	120
CCTGATTTAA AATCATGGCA TAATTTGATT TTCTCTGTCT CACCATCATT GCAGGGGCAT	180
TGTTAGTATG AAAATGAAGT TTAATAATAT ACGCTGGAGG AGGTGAGCAC CCTGACAGGC	240
AGAGTTCTGC TCTGTGGTAA GACAGGCCAG GTTGGGATGC ACCGTGTGGC CAGAGTGCTG	300
GATGTGCATC AACCTGTGCA GTGGGGACAG CAAGAGGAAG TGAAATTAAA CGCATAGATA	360
GACGACAAAA CTAATAAAAA CCAAGTGCAT CAAAACACAG TGTGAAAGTA AAAATAAAGT	420
GATAGTACAA TCTCGCTATA CACAGAAATT CTAGGAAAGG GAACGGCCAG CCCCTGGGTA	480
AAAATTCCTT TGTTCACTCT TCCAGAAATGA CAGAATTTGT TGAAACATCT TGCCCTTTAT	540
GTGTGGGAAT GTAAAAACCT CCATTTTTC CCATCACCCCT TTGCCTCTCC ATTCCTCTCC	600
TCTTATCTCC TCCAGTCTGG	620

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

GGGGTGCTGA GGCACACGCT GGCCTGTCCT AGGCACATGC CCCTGATGGG TCTGTGCAGT	60
ACCATGCACA TCCTCCTAAT GGTGGAGGGA GGACTTGACA GAGGACTGGC AGGGGCAGGT	120
GAGTGATATC AAACAGAGCT TGGCTCCAAA GTCAGGGGCT TGGGTGGGAC TCGCCTCCAT	180
GTAATCTCTA AAATATGGTC TTAGGAGGTG AGGAATAAAT GCCTAAGTGA TGGGAGAATC	240
CTCTGTAAAC CCAGAAGTGG GTTACACCTA TTGGGAnGGT GGTGGTGGGT GCCCGGAATA	300
AGCTGGTTTC CCAGCAGTGC AGTGGCTCCC ACCCCTCATC CAAGGCTCGC AGGAGTGTCT	360
CTGGGCTGCA TCCTGTGTGG GTCAGGATTG AGCATCGTCC AGCTGTGATC AGGCATCTGG	420
GATGCAGGAG TGAAAGGATA GTCCTTGCCC TCTTGAAGCG TCATCGAGAG GGGACAGATA	480

1018

GTGAACAGGC CACTTTAAAG CAGGACAATG TGATGAGGGC CGGTGGAAGT GGGGAAGAC 539

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

GTCTCCCTTG GCAAAGCTGA GGAAGCCTGA TTCCTCCCC GCTGCCATGC AGAGGTGATG	60
GGGTCGCATG AGGATAGAAA GAGAACATTA TTGGGTGAT CTGTAAGCTG TTA TCTCCCCA	120
CTGAAGAACA GGCCCTGTCC CACTCATGTC TGCCACCCG CCTTCACCTT ATCACAGCCT	180
TCCACACAGA CGCGGCCCC TGAGTGGGCC GCTCATGCTC CTAAGCCTGC TGTGAGGGCC	240
TCTCTGATCC CTCCGCCCC CACTCTCCTC CTCCTCCCTC ACCGCACCTG TTTTGGGCAG	300
TGCCAGCTGT GCACTTCCTG GACCTGTTGG CTCCCTCCGG CTTTACTCAC ACTTCACCTC	360
CCTGGGCCCC AGCTCCACGA AGACCTCTCT GCTGAGCCCC CATGATTCTT AGGCGTCCCT	420
GCTCCTGTGC TGTCCCCAGG GCCCTACTGG CTCTTTCTTG ACCCCCTCCC TACTGAAGGC	480
AGAGCAGCTG GCAGTTCATC TTTGTCTTTC CCTCCTTTGA CCAGGGGCCT AGTGACTCAG	540
AGCCACAGGG CGGTTGTTCC GGCTGCTGTC AACTGCAGAT GGAGATGTGG AGA AACTGA	600
GGCTGACCAC TGGCCTC	617

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

CCTCTCTn C ATTCTGCCTG TTCAAGTAAA TAATCATTA AAATTTCTC TATCAGGGGC	60
TGGCACTGTG TCACAGCGGG TTAAAGTCCT AGCCTGAAGC GCCGGCTAGG ACTCGAACCG	120
GTGCCCATAT GGGATGCCAG CACTGCAGGT GGAGGCCCTG CCCACTACGC CACAGTGCCA	180
GCCCTGCAAA GTATGTTAAA AGCAGAGTAC ATTTGGGAGG AGTGAGAATG GATCTCAAGA	240
GACAGGTTAA GGCTGTCCTT TTAGGGAGAG CACTTATCCA GGCCAGAGAT GGTGCAGCAT	300

1019

GGACCAGGAT AATGACCAGT TACATAGACA GAACCGAGTA ATCAGCATCT ATTTTCAGAAA	360
CAGAATCATC AGGATGTGGT GATGACTTGG TTGTAGGCGT GCAAGAGACA GGGTTGTTGA	420
GGATGCTTCC TAGGTTTCTA GCTTGAACAT TCGAGAGACT ATGATTAAGA GGCCTGTGAG	480
AGGTAAGGGC AGGTGTGTGG AAAATTCAAC CCTTTGCAAT AAGCTGCATT TGAAATACTT	540
ACTGAACATC TAAACTGAGA TGGCAAGGAG GCTAATGGAT ATGAGAATGT GTAAATTTGG	600
AAACAGTCAG CAGATG	616

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

CGGTACACCC ACAATTATTA AATGACATTT TTTTCCAGT GCAGGCTTTT GTAGAATTTG	60
GGTAGATTCT ATGAATTCCC AGACATCATA CTATGACCAC TATATGTATG TGTGTTTATA	120
ATCACATGTG TGTGTGTGCA TGTTACTTTG TAGAGGGAGA ATACATAGCT TTTCTCAATA	180
AAATGCATAT TGCAACAGAA GAAGGGCCAA AGGCGTATTG GCCTCAAGGC AGCGTGATCT	240
ACTAGAACTA AGCCTCACCA AGAGGTTGAG AGATTTGTGC CTTTGTGTCT CCGGGGACCA	300
CTAAGCAATT GTTTGACTCT AGGCAAGTTA CCTAATCTCT TCATATCTCA GTTTTCTCAA	360
CCATGAAATG GAGGAAATAA TACCCTGCAC CTGCTGTTT CAGCTCATAG GGCTATGGTG	420
AGGATCAAAT AAGGAATGGT AAGGAAAAAC TTGCACTGA AGAGTTCTAC ATATGCATGG	480
TTTAGGAGAT TAGGCTCTCC TGCTCTTCCC CACACCCCC TCACCTTGCC CACCCTCAAA	540
AACTCCCTGT GAGAGAACCC GGCTCTCACT TTCAGGGAAT TTCCTCACTT CAAAGTAAAT	600
AATTATCAAT ATnTnCTAAA TTTTCACATT TCTCAGTTAT CAGGGAATGT TATTTAGGGC	660
TCTGCCCCATA	670

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

CTATCCTACC TATCAGTAGT ACAATGAGGC ATTGCCCAA AATGTTGGAG GAACAGATCT	60
CAAGGGAGAG TACCCCAAAC CTTCTGCTGA TTGGTAGTTA TAAGTCATTT AGATAGTACG	120
GTGGGGGAG GTGACAGAAC TCTGAGCCCT CAAGTCTAAA CCATGGGCAG TGAAAAATCC	180
CATGTGAAGG ATTTTAGCCA CTCTATCTTG CTGGAGAGGC TTCTAATCTT CCCCCACCCC	240
TTATCCACTA ACACCACAAA CACCCAATTA TTTTCTCTT ACTAGTAGAG GACCCTAATT	300
AGGCTCTAAT TAGCATATGA ATAGAGGAAA CAAGAAGGGA GACTGCTTTT AGTGCTGGAA	360
GCTGCTATCC CAGTGATCTC TTAATACTTC CTGATGCTAG AAAATCCCTG GAAAACAAGA	420
ACACAAGGAT TAGGCCACAC TAGCCCATTT CAGGGCAGGT TAAAATAATC AAGGTAAGCA	480
ATGTGCTTCT TCCCTTAGCT ATACAATTTT GATATTATCT TGGAGTGCTT TTAATTACAA	540
TTGAATATAT ATATATnTGT GTGTACTGGT GCTGTTAGAC TAGGACTGAA CATAAGTTTC	600
TCAAACAGAn GCATGTTTGC AAAAATCTCT AAGGAATC	638

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

GTCTGATCAA AAAAATAAAA TTAAAAAAA TAAAAAGAA TGCATACTAT GAAAAGCTAT	60
GCATAATTTC AATATTTTTT GCACAAAAAA ATAAGTTTAT CCTTAATTCC TATATTCCAC	120
TTTTCCACAG ACATTTTGGC ATGCCCTCAT GTAAC TGACA GAATCCTAAC TGTGCTCATA	180
GCACCATATT ACTGCTTGCA ACAAGCAATT AGTAGCAACG GTGCTGGAGT GCAGCATTAA	240
GCCAATCCCT GCACTCTATA AAAAGTTAAA GGGCACATGC CCAAGCAGGC CCCTACATGG	300
GCACAGATGC CTGAGAGGGA AGAATTGTAC CGACACAAC CTGACCCTCC AGACCTCCCA	360
AAAGGCAGGG TGGGGCAGAA AGCGGCTCCA CTTAGGAGGA AGATCAACTA CTTTCTCTTA	420
CACCATGGTG AAGAAAGTAT AGGAGGCTGC AGACTGTTTG CCTGCCATAC TTTCACGTTT	480
CAAAAAGAT GAnAACCATC AAGCCTGGGG GAGAGAGGTG CTCAGCAAAT CGGGTGnAAT	540
TAAGAGCAGA GACGTCTGCC CAGCTGTGGG CACTCA	576

(2) INFORMATION FOR SEQ ID NO: 517:

1021

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

```
CCACCCGTGT TCTTAAATTT TTCTTGATTT CCTAATTATC TATTTTGCTT TTGGGCTTCT      60
CTTTTCCATC ACTTACCATA ATATTGAGAA TTTAAAAAAA ATTAGAAAGC AGGAAGCTGG      120
AATCAGGAGT GGAGCTGTAT TTTTTTTTAA GGTTTATGTA TACACACACA CACACACACA      180
CACACACGGC GGGTGGGGAG AGAAACTCAG AGTTGGACCA GGCTAAAGCA AGGAGCATGG      240
AACTCCTTCC AGTCTCCCCA TGTGGATGGG CAAGCGTCCA AGCGCTCAGA CCATTTCTTG      300
CTGGTTTTTC AGGTGCATCA GCAAGGAGCC GTATGGGATG TGGAGCAGCC GGAAGTCAAA      360
CCAAAGTTCA TACGGATGTG TAGGCAGTGG CTTTCATCTGC CGTGACATAG GCCAGCACCT      420
GGAGCTGGGA CTTGAACCAC ACATCCCAAG CAGCATCTTA ACTTCTACAC CAAACGCCTG      480
CCCCTCTTAT GGTTCCTTTG TTAATTGTCT GAAAGATACC TGAAGGGTGC GTTCCATCAC      540
AGATGTGGTA TTACAATGAA TCCTTCTGAG GGATATCACn ATTTTTT      587
```

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

```
AATGATGGTG TAGGTCCGTT CAAAAATCTT ATGCCACAAA CAAAACACAG CTCTAATTAG      60
TATGTGATCA TAAACAAGGT AAACGCACCT CCCTAAAGCT GTCTTAAAGC CTTTGTTGTG      120
GTTCACTAGC TCAGAGAGAC GCTCTGAATT CTGTCTCCAT GCACTGTACC AGGGCAAAGA      180
TGTGGCATTG TCCAAATCTC ATCAAGAGGA TATATCTACT GTAAGGnAAG AnTGTTCTGC      240
AAAAAA      246
```

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1022

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

TGTGCCGGCA GCCGGCGCCG CnGGAAGnGG ATTAGCCTAG TGAGCCGCGG CACCGGCCCA	60
TAGTTCCTTA TTTTGAATG GGAATGATAA GTACCCATCT GATAGGGCTT TTGTGAGGAT	120
GAAAAGAGTT GGAAATATTA AATCATTACT TAGGGGCTGA CACTTTTTTT TCTTTTATGA	180
GTTGTTTATT CCAAAGACAG ACTGACAGAG AGGGTAGAGA GAGAGTGAGG TAGAGAGAGA	240
TCTTCCATTC GCTGTTTCAT TCACCAGATC ACCACAACAG GCTGGACTCA GTCAGGCCAA	300
AACCAGAAGC CAGGAAGTGC AGCCAGATCT CTCACATGGG TTCAGAAGCC CAAACAGTTG	360
GGCCATCTTC TCTTGCCTTC CCAAGCACAT TAGCAGGGAG TTGGATCAGA AGTGAAGCAC	420
CTGGGGACTC CAGCCGGCAC TCGTATGTAG TGCTGGCATT GTGGTTAGTG GCTCAACGTG	480
TGCTGCAGCG CCAGCCT	497

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

AGCGATGATA TTTTCTTCAG CGCGTGCCT ACGCnTnCCC ATTCTGCTGA TCTTCAAAC	60
GCGCAAAAGA ACTCATCGCA GATGAGTnAC AACTCGTCCA ATTTACTCAG ATAATAGCTG	120
TCACGTTCTG TCAAACAGTC ATCAAGAAAC TTTGCCTCCG TGATCACTCT GCGCGCCGTC	180
TGCCCTTCCA TATAAACTCC TCATCCCCCA ATTCACGTTT CTCGCGCGTG TGCTATACCC	240
TACACCACTT AnAGCGTGAG AGAAAGCTTA TACGCAGCAC GCCGCGCGTA CTCAAACGCA	300
GGACACTTTT CTGCAAGGTT GTAATACATA TCACGCGCCT GGGCGTGCAA ACCCTTTTTG	360
TATAAGAGAT CTGCAAAATG GAGCAGTGTC TGCCACACTC CATGCTCnTG CGCCCACTTC	420
AAAATAGTCG GATGAGATCC AGTTCGCAAA AATAAATCAG CAAGATCCTA TACTGATA	478

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

CCCGTTAAGG CCAGCTCCCC TTCAGTCCTC ACATCTGGGG AGGGTCACCA CCAACTCGGG	60
AGAAGTTCTA CTTAACATCC AGCTTGTAAC CTTACTGCTA TTCACGTTCA TGTCCACTGT	120
CTTGATTCTG GATAAGGACC CTTAGAGCAT TAGAAGAGGA CAGCTGTCCC GATGGGCACA	180
CCAGGCTGTC CTCCTTCTGT ATAAGTGGCA GCTTCTAAGA GCTATGGCCT ACGCCCAGGG	240
AGGGGCCTGG CAAGTGGTGG GCACCAATGT ATGTTGAAAT AATGAACGTG ACTGCATGCC	300
TCCTCTCTGG GCACGCCTGG CTTCTCTCAG GCCTCAGTCC CCGGCCCTTT CCTTAGCCAC	360
AGGTTGGCTC TTCCACCCCG GACATAGCAC AGCACGTTCC CCTTCCCTGT CTAGTCCTGA	420
GCTGAGGACG TGGGGAACGG GGCCCAGGTT AGGCATCCAC ACCTCCCATG TCAGACTGAA	480
GCTGTTACAG TGTCATCTCA GGGACTGCTT CCCTGTGCTT AGTCCTTAGG TACCAAGGGG	540
GCCTACGTCT GGGAGAGGAG AAGCCCAAGA GTCCCCAGCT TGGGGTGCCT TGGGCCCGTG	600
GAAACCCCGG CCCACCTGCA GGAAGCGAT GCTGAAGCCC TGAGCGC	647

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

GAAGCAGAGG TGCAGTGTCC CGGAGCCCTG CCCGCCCTTG TGGGCCTCTA AACTAGCTC	60
CTGTCCCGGC CCACCTAGAG CGCCCTGCGG TTGGAGGACG GAGACCTGGA GGAAGCCGCA	120
GCTGCTGCAG CTGCAGGTGG GCGGCGGGAG CGACGGAAGC CGTCTTCAGA GGAGGGCAAG	180
AGGAGCCGCA GATCTCTGGA AGGCGGGGGC TGTGCTGTGC GTGCCCCAGA ACCTGGGTAA	240
GCATGCATCC GGTAGATGC GGAGGGGTTG GATCCGCCAG GCGGTGGCC CTGCGCTCTG	300
ACAGGCCCCG CCTCCAGCCC CACAGGTCCC GCCTCCCCGA CAGGCTCCTC CTCCTCCGTC	360
ACGAGCCCCG CCCCCTGGC CGGCCGGCT TCCAGCCCTG TGAGCCCTGT GAGCCCTACC	420
TCTGGCCTCC GTACCTCCGT GAACTCTTTC CTACCATTTT CACGGCGCCG TCAGGG	476

(2) INFORMATION FOR SEQ ID NO: 523:

1024

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

TAGTATAAGC CAGAAAAGAA CCCAGAACTG AGAACCCACT TTGCAGACGC TAAATTTAGA	60
ACTGCCTGAG GCAGCCTCTT TCAGTCAACT TTCGGGTAAA TTTTCTATGG CAAAATATG	120
TGCATTGATT AGACTTTTTA ATCCATCCGA GAGCAAACAG TGCTGACACC TTGACTACCG	180
GGGTCCTCAT CCCTAGCCTG CGTTGACAGC CTTAGGCTCG TGTTCCCATATA ATGTACTCAA	240
ATCACACGCT TCCGGGCTGC GAACTACAAA CCCCAGCATG CATCACTTCA TCTTCCACAG	300
GGGnGGGGG GCGCCTGCC GGGGACTGTA GGCAGCCGCC GCTCTGGTGA GTCCAGCCAG	360
GGACAAGAGC CTTTGGGGGA CACGTCCCAA ACGGGCCAGC TGCGGACTCG GAATCCCGTT	420
TGGCCGCCGC CCTGCTCCTG GCAnCCGCAA CCTCCGACAA nCGCACCCCC AGCGGCG	477

(2) INFORMATION FOR SEQ ID NO: 524:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

nCCGGGCGAn CTCGAGCGCG AACAGGCGGC CCAGGCCGCT GCCGGCGCCC GTGATGAGGC	60
AGACCTGGCC GGCCACGCTC TTCTCCTTGG GCCGCACCAG CCAGCGCGCC GCGGnCCAGC	120
ACGAATGCCC ACAGCACTTT AAAAGTGACC ACGAAGAACT CCACCACGAT GTTCATCGCG	180
ACGCCCAGGT CCCCnGCCA GTGCAGCGCC CGCGTCCGCA CCCAnCCCGC GCCGGGCAGC	240
CCGGCTCACC GCCCCGGGGC GCTTGT	266

(2) INFORMATION FOR SEQ ID NO: 525:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 587 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

TGCCAGTGCC TACTGCTCCA TCTGGTGCAG AGTCTTTCCC CAGCTACCTT TTGATTCATG	60
CTTTTAGACC ATTCAGGTAG CGCCACTAGA AATTATTTCC TGTCTTCCTG TTCCCTCCCT	120
GACAGCCGGC AGCTTCCCCC TGTGGCGTTC TCTGTAGTTT TTATCACGGC ACTTCACATT	180
CATTTTATAT ATATCTTGCC TTCATCATCA AACCCGTCTT GGTTTCACCA AGACCTAACC	240
CAGTGCTCGA CAATGACAAT GAATGTGTAT AAATGAATGT CGCAGGGACT GGCCTTTTGT	300
CCTnAGGTTA AGATGCTGGT GTCCCATACG GGAGTGCCTG AGTTTGCTGC CGGCTCTGGC	360
TCCTGATTCC AGCTTCTCAC CAATGGCAGC TGCTGAGAGG CAGTAGTGAG AGGCTGTAGT	420
GATTGAGTCC CTGGCCACAC ACAGGAGACC GGGATTACGC CTCTGCCTCC GAACTTCAGC	480
TTGGCCCATT CTGGGACATT GTGAGCATTT AGGGAGTGAA CTGGTGATG GAAGTGTGCA	540
CACACTCTCT TTTTCTCTCT GCTTCTCTGG TGGCCnCTCC TCCCCTT	587

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

TTGAAAAAGC CAGGAGAGAA TGCTGGCTTA GAGTTTCTCT TATCATCAAA AGAGCAAGGA	60
CGAGGGCTCC CCTCGCGTTG CCTGGGGATT GTGTGGCTGG AATCCAACCC CTACTCCTGT	120
CTCTTTTACC AGCATCAAAA GAGGAAACAC TTGCTTTCAT TTCAGCTTTC CTAGATGTGA	180
GGCCAAAGGA GTGAGAGTGG GGAAGAGGGA AGGGATTGTA AATTAACAAC TGTTAGTAGT	240
GAAACATCGG ATGGGATGCG ACTCTTTATT ATAATTCTTG AATATTATTT CTTTTTGCCC	300
GTGTGAAATA CTTTTTCATA ATTTTATATT TGGATTGTTC ATTGTGAATA TATAGAAAGT	360
CACTTGATTT TTGTATGTTG CATTTCATTG TGCACCTTGC AAAGATCTTT TATTGGTTCT	420
AAGAGTTTTT CAGTGAACCT TTTTGGGATT CCTATATACA AGACCATGTC TTCTGCAAAG	480
AGAAAGTTTT GCTTTTTGTT TCTGGGnTTC ATACTTTTAA TTTTCnTGCC TAATGCTGT	540
GACTAGAACA TCACAGACCA T	561

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs

1026

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

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CTCGCCGTCT AAATCCCACA GGAACCGACT GTGTCCCAGG CACCCCTGCA GGGCTCTGAG      60
GGTCCTGATC TCTTCCTGGG ACCCCCACAC CTCCAGCGGC CAGGGAGAGG CCAGGAAGGA      120
GGGAGGAGCT CAGGGACGGG GTCCATCCCT GGCCTGCGGT GGGACCCCGC CCAGCATGGA      180
CGCCATGGCC AGCCCGGCAG TCACGGGGTG CTGCTCCCGG AATCCTGGGC CACCAAnCCCG      240
TCTCCCCCA CnCTCTTCT CCCCCACATC CCTACTGCAA GGCCCGGGGA GGGGCACACC      300
CTGGGGAGTT CAGAGGATGG ACAGCAGGTG GCCCAGTGGC TCCCAGGGAT AAAGGGnAGC      360
TnGGCGTGGT CCGA                                          374
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(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

```
GTGCACATTC TCTATTCACT TTAGATCACC TCTAGATCAC TTACAATACA TCACAGAATA      60
TAACTATAAA CAAGTAGCTG TATTGTTTAG GGAATAATGA CAGGGGAAAA ACACGTTTAG      120
TACAGATGCA ACTTTTTTTC CCCTAGATAT TCTTAACCCA AGGTTAGTTG AGCCATAGAT      180
GTGGAATTCA CAGAAACTGA AAGCTGACTG CAATCAGTTC TTGCTAACAG GGCCTGCCCT      240
CAGAAGAACC TAGTTAATCA GAGAAAAATC TGTTCAGGG GTATTCTAAG AGCATAACTG      300
ACAGAGAGAA GGGAAATACC CAAATCTAGT TAGCTCTAGT CATCCTGTCT CACCTAATCT      360
GGGACAAAAT ACTGACAAAC AACTGTGAAT ATCCTCTTCC AAGAAACATT AAGTCCGAGA      420
TCTAATCAGA GTAGTATAAA ATACTTACCC TGTCATAAA GGACTATTTA CATAATTCCC      480
TTTTACCTGT AACATCACAT CCAACTAGCA AGAAGAAATT ACAGGGCTGA CATTGTGACA      540
TTATGGATTA AGCCACCACT TGTG                                          564
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(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs

1027

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

CGGATGCAGC TTGTTCTCT GCATGACGGA TGAATTGATG GTGCAGCCAG CCTCTTTCCT	60
GAAATGATAG GCCACTGTCT CCAGAGAAGC TTGTCTATGA GTGGCACTCC ATATCATCCC	120
CAGCTACTTT TGAGATTAAT GTGACAATGT GTCTTTGCTT CTTCTCAATG AATTCCAGCA	180
CTGTAAGTnT GTnTAGCTCT CCTAGTATCT GGAGCTGCAG ATTTCTGCAG CTCTGGGTAT	240
GTGGAGGACA CCCCTGCCTT CAGCAGGACC GAGTTAGGGC TGGGGGCTGG AGGTCAGGGA	300
GTATATTTCC AGTAGCCCCA TAGCAGGATG TTAATTTACA AACAGCTGGA ACTTTCTCGG	360
GGAGCACAGG GGCATCTGTT TAGGGCAAGG ACACCGTATG TGTGTGAGGC TAGAGAAAGG	420
GCGGCTGGTG GCAGGAGCAT GGTGATTGGG TATAGTGTG CTGATACAGG CTTGTGCAGA	480
GAGGGCTGCC CGCCCTTGGC CAGATGCAGC CTGTAGCTGG TGCATCCC	528

(2) INFORMATION FOR SEQ ID NO: 530:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 416 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

TTTTGTTTTT AAAATGGAAA TGTTTCTTAG GGGTTTTGGC ATGCTCTTTG ATATGTTGAA	60
AGATGAGAAA ACATCATTTG GAAACTCAGC ACTTATACCA TATTAGGAAA TTTGCAGTGC	120
CTCAGATTTT ACATTTAATG TTTTAATTGC CTGGTTTGGG AATAGAAAAC TTTCAAGCTT	180
CTCTCTTTCA TTTGGAATTT CCACTGCTAA CTTCCCCCTC TGCAGTGGTG GGCTGCTGCC	240
TGCCCCATTT CCTGCCCTGG TTCCAGCATG GACCAGTGGT TGCAGAGAAAG CAGTTCATCG	300
CATGTCATCT GAAATGAATA TCATATTGAC TTCCGACAGA CTGGCTTACT CTTTTTTTGT	360
GATACCACAC ATGCAGTTGT TTCTGTGGG ACTTGTAAT ATCCTAAAAG TGCAAC	416

(2) INFORMATION FOR SEQ ID NO: 531:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

1028

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

TGCACACGTA TGGGCCGCCC CAACACAGCC GCCATGACAT TAAGTGTCTA GAGGGAATAG	60
ACACAGGTGA ACACATGTGG GCCGCCCCAC ACAGAGACAC AGCCGCCATG ACAGCGTGTG	120
TCAGGGAGGG AACAGACACA CGTGCACACG TnGnGACCAC CCCAACACAG CCGCTATGAC	180
AGCGTGTGTC AGGGAGGGAA TAGACACAGG TGAACACGTG TGGGCCGCCC CACACAGAGA	240
CACAGCCGCC ATGACAGCGT GTGTCAGGGA GGAACAGAC ACACGTnCAC ACGTTGTGGC	300
CGCCCCACAC AGTAGACnCA GCCGCCATGG ACA	333

(2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

AAATACTCGA CATATTTAAA AAGTCTTTTC ATTTCAATTC AAAATAACAG TCTCTACCTA	60
CTCATGAGCT TCCCAAAGTT AAGACTTAAC AACATTTTGG AAGACTACTG TGAAC TTCAG	120
CTAGCTTTAC TAAGATGTTT ATGTGTTGTT TGGATTAATT TTGACCAAAG ACCTGTATGA	180
AGTTCAAGGC TGATCCTCTT ATGATGACGG TCATTCTCTGA GCCAGCCTGT TATGATTTTG	240
TACTTATCTC AAGTGTA ACT TTA CTACTACTTT CTATAACGAG CAGAGTCCAA ATGCTTGGCG	300
CTTGTTTAGA GCTTTGTGCT GCGCCAACCA TCCACCGCTA ATTCAGATAA TTTGTTTCAGA	360
GAGGTTAGAC GGCCATCAAC TCCATAGAAG CTCCTCCGGT CCCCCAGAT CACAGAATTT	420
TGGCTTGCAC TTCTAGAAAC TGCCCAAGGC CTGGCACACA GTAGGCACTT AATTGTTTAA	480
TGTTGTTTGG GAAGGAAGTA GAGAGGCAAG GAGGGAGTTG GCAAGGGAGG GTGATGTGGG	540
AAGCCGTCCT GAAAGAGCCC ATTCTGACCA TGGCCGTGTC TGAATCGTAG ATTACAGCAG	600
AGAACGCGCG TGGATC	616

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

CATCTTTGTC CCTCTGACTT GTCAGTCTGT CCAGGGGGCC ACATCTGAGC TTGTAAATTA	60
CCACTCTACC CTCTCTTCCC TTTCTGCCAC CAACACCCTT GCTCTCTCCT CCCAGCCCTG	120
TGTGGGGAGC CAGGCTGGGC ACCTCCCAGA AAGGCTATTG GCTGTTGGCT GCTCTCTGCC	180
CAGGCATCTC TGGGCAGCCC AGCATTGGCT TCTGCTGCCT CCTGGAGGTG GAAGCTCCTG	240
GGTCCGTGTC CTGCCTGGTT GGACCCGTGA ACAAGCCAGT CCCTGTGAGG GTCTTCCCTT	300
GGCAGGCCTC TGGCTGGGAA GAGGACTCTT GGCAGAGTCC ATGAGCTACC CTCGCTGGAA	360
CTTGAAATTC CTGCCCAGAA GGGGATGGCC CAAAGCTGCA GGAAGTACCA GGTGCAGCGG	420
GGCCCCCTGGG TACCAGGATG CCACTCCCAT GCCATCTGCC TTCCCCGTCT GACCCCTGCTT	480
CTCTGCTGGA ATGTTGCCTT CAGTTTTTCA GACAGCCCTC TTCACACGTA TGCTAGAAAC	540
ATCTTCCCTG GGGGTCTCAC AGTTGCATCT TCTTCCTCAn TCCCAATTCA GAAAATCCCA	600
GGGGAGCTTC TCATTGGGTC CATTTAGGGC CCATAnA	637

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

TTCTACAAGT CCGGCACGTT CCGTTATGAG GATGTGCTCT GGCCGGACTG ACCAGCGACG	60
AGACGAAAAA ACGGACCGCG TTTGCCGGAA CGAATACAGC ATCGTTTAAC TTTACCCCTC	120
ATCACTAAAG GCCGCCTGTG CGCTTTTTTT ACGGGATTTT TTTATGTCGA TGTACACAAC	180
CGCCCAACTG CTGGCGGCAA ATGAGCAGAA ATTTAAGTTT GATCCGCTGT TTCTGCGTCT	240
CTTTTTCCGT GAGAGCTATC CCTTCACCAC GGAGAAAGTC TATCTCTCAC AAATTCCGGG	300
ACTGGTAAAC ATGGCGCTGT ACGTTTCGCC GATTGTTTCC GGTGAGGTTA TCCGTTCCCG	360
TGGCGGCTCC ACCTCTGAAT TTACGCCGGG ATATGTCAAG CCGAAGCATG AAGTGAATCC	420
GCAGATGACC CTGCGTCGCC TGCCGGATGA AGATCCGCAG AATCTGGCGG ACCCGGCTTA	480
CCGCCGCCGT CGCATCATCA TGCAGAACAT GCGTGACGAA GAGCTGGCCA TTGCTCAGGT	540

1030

CGAAGAGATG CAGGCAGTTT CTGCCGTGCT TAAGGGCAAA TACACCATGA CCGGTGAAGC 600
CTTCGATCCG GTTGAG 616

(2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

CCCTGGTCTC ACTCTGTTTA TGGAAACCAG CATTTTCCCC TCCCTTGTGT TGTTTCCCTT 60
CCTCCCTTCA TTCTTTCCCT CCCTCTCTCT CCTCTTTCTG TCACTCTATC TTTCAAATAA 120
ATTTTAAAAA ATGTTTAAAA GGAATACTTC TGTAAGGATG TCTGTCCAAC ACCTGCGTAA 180
CCATGTACTG GTGCCATCTT TGTTACTGAT CCTTTAGCAC ACTTGTACC AATCCTTGTG 240
GTCAAAGATT GTTGTGTCAA AACAACTTAT GTAACCTTCC CCACGTTGTC TTTAAAAACA 300
CCCTTTGCCT CAGCTTTTAT GAATATACTC ATAGTTTACA GTGACACAGG TGCCCCCATT 360
GCAATGTCAT GTGATTCTCA GACAAACTTT TTGAATTTTG GAGAACTGT CTTTGTAGGT 420
TATTTAGATC GACAAAGTTT ATTC TGCTAT GATTTGTATT CTTTTAAATT TGTAAGTTT 480
TAATGGCCCA GAATATGGTC TATCTTGATG CATGGGCACC TAAATTTTG AATTGTGCGA 540
nCTC 544

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

TTTTCTAACC CTCTTATACC ATATCTACCC CTCAACCTTT CTGAACCATG CTTGAGTTCT 60
AGCAGTCACG TTCTCTGTT TTAGTCCTCC ATGATGTGCT TTCTGACTGG AACGTTCTCT 120
GCATTGTCTT TCTTCAGACC TCAGCTTCCC CACCCCTTCC ATGAGAAAAC TGGTGCTTTA 180
CACTCTCCCC ACTGCATAAT GCTTGCTTGA ACCTCCTCCT AGCTTCTACT GAGTGATTGT 240
GTCTTGGTCA TATGTGAATG TCTAGTTAGT GCCTAGCACA ATACTTTTCA TGTAAGTAAAC 300

1031

CATCTGTGAA	TGTTGGTTTA	AACGAGTTTC	TGACAGTTTT	TTTTGAGTAC	TCTTCCAAGG	360
CCTAGTTTTTC	TTGTTTGTGG	GAAGTCAACC	AGAAGAGTAG	GAGTTGGAAG	CAGGCAGACA	420
AGAAAAGGTT	CTTACTGGCT	CCAGCTTTGC	ATGCATTTTT	TTTCCCCTCT	TCATTTCTTT	480
CTTCCATAGC	ACCGTTCAAA	TTTGCAATCA	TTTTACTACA	CTAGTCTTCA	CAGACCTTCC	540
AGGCACAGAT	AAAGCTAACA	GAGTTTTAAG	GCAAATGGTC	GGTTCCTGCA	CCCAGCTGTT	600
AAGAGGGCTG	CAGAGTGTGA	GTGAAGACAG	CTGAAGTGGn	TAACATAATCA	AAGGGnATCA	660
TTCTCTCTGG	CAGGACA					677

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

AATTCCCGGC	TTCAGCTGCT	AGGGGCATTT	GAGGGAGTGA	ACCAGCGGAT	GAGAGCTCCA	60
TCTTCATCTC	GATTTCTCTC	CCTCTTACAA	TTAAAATTTT	TTTAAAGGTA	ATTGATCATT	120
GTTCTGTATT	TCTTTTGGTT	ACAGGTGTTT	TTAAGTTCAA	GAGATTTTTT	TAAAAGTAGA	180
TACTGCAACA	CGTATTTTTA	CTACGTTCGC	GACTATTTTC	TTAACAAGAG	CCATCTGCCA	240
CTGATTAAAG	ATCTTTCATG	CATTATAATT	ATTGCAAGGG	ACTTCCCCAA	TAAGCTTAGA	300
AAAGGTGTTG	TGACTTCTGC	CGTCTGCATA	AAAGCGGGAG	AACGAAGCCT	CAGACGCATG	360
AACCGACGCG	GCCAAGTCAC	AGGTGCAGGA	GAGGTGTGGA	TTCTCATTCC	GGCGCCCAGC	420
CCCACGCGA	CTCCTGCGGA	GGCTTCTCTC	ACCCCAGCAG	AGCCACCATT	AGCTCGCCGG	480
GCAGCGTCCG	GGCCAGGTTT	AGCCGCGGCG	CCCCCGTGAG	GCTGACGCGC	TTGGTTGTTA	540
TGACGACACG	AAGGGCAAAA	GCCCGGGGAA	AAGAACTTTG	AAGGGCATTG	GCGGAAAGCG	600
CTCCCCACCC	CAGGT					615

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

TGAGTTAAAC AAATCTCTTG TCTATAAGGT TGGCCTGCCT CGGTTATTTC ATTATATCAG	60
TAACACACTG ACTAATGCAT ATACGCAGAT ACAGGACTGC TGGGTCATGT AGGAATTGCA	120
GCTGTAATCC TCTGGGGAGC TGCCATGCTG TTTTCCACAC AGCTGCAACA GTTTCGGCGA	180
TGTACCAAGG GTCCCATTTC TCCCCATCGG CGCCAACACT TGCTGTTTTT CGTTTGTCTG	240
TCTGTAGGGG CCATCTGCAT GAGTGTAAGT AGACCCTCAG TGTGGTGATT TGCACCTTCTT	300
TATGATTAGT AAGTTTTTTT CATGTTTTAA AATTTTATAT ACTTGTTGGT CATTTGCATA	360
TCTTCTGTAG GGAAAATATC TATTCAAGTC CTTTGCCCAT TTAAAAACCT AGATTATGTT	420
GTTGTTGTTG CnATATAAGA GTCCTTTATG CATTTCTGGAT ATTGATCCCT TATGAGATAC	480
ATGATTTCTA AGTACTTTCT CACATTATTC AGGTTACCTT TTCTTTTCTT TTAGAAGTT	540
ATTnATTTan	550

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

CATTTATTTG GTATGTCATT TTCCCCATG TGCTTGCTGC ACTACCCTTG CTACTCCATC	60
CCTTAAATCA CAAACACATA TGTACCTGCA TCCATCCCCA CTCACATTAT ATTTCACTTT	120
TACTTCCATC CACCCAATGC TCGATTCTGT TAATTAGTTT TTTTAAAGAT GAATACTACT	180
GAAATTCCTG TTAAGTCTTC TAGCAAATA TCAGAAGCCC TAAGGACAAT GAACTTGTTT	240
CCCTGAACTG ACAAACCTCA ACTGAAGCTG CACTAGAGTC AGCTCCTTTA AGGTGTGACC	300
ACTTCATTCA TCCATGTTGT CTGGCTGGCC CTTGGACATA TTAAATTTTT TTTTACTATC	360
ACTCTTCACT TGTTTGATC TTGACCTGTC AACACTTCAT TGGAAAGTTG GTAAGGAAnC	420
AAACCAAAAA AAACATGGTA GGTAAGTATC CCCACCAA	458

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

CAAAAGTACA GGAGGAGTAG AGGGACGATG ATCTGTCTTT AGAGTTACTT CCTGCTGACA	60.
TGGGGCAATG AGGTACTCTT CATTGGCATG GGGTAATGTC TCGAGCAGCT GTCTCCTGGG	120
TTGGGAGCCG AGTATATCCC TGTAGCAGCA TTTGGTTGAC TGCCTGGTTG CTGAAGGCCT	180
TGGTTAGCTC CATTATCAAC TCTTTTAAAC ACTTAAACAG ACATGGTAGT TTAAAAGACA	240
GGGTGAGAAT AGCAACAAAT GATCCTAAGA GTGGCATTAA CCCGGTAATA AGAGGATTTC	300
ACAGAGGAGA GGAAACGAGG GGGGTGGTCT CTGGACCCTT GTGATGACTG TTTGATGGTT	360
TAAAGCTTAT CTCACCCAAG ACTGGGAGAA AGGCCACTCA ACTTTTGCAA GTAGAGGGGT	420
TTGTCTGTAG AGAAATTCTG AACAATCATT CAACATTA	458

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

AGGGCATGAA AGGCTGTTCC GGCCACAAAA TAGAGACCCT GTTTAAATCT TATTAAACAA	60
TAACGCCCAC CCAGTCCTCC CCTCCCCCCC TTTGGAAAAA AATTCAGGAA GGAAATTGTG	120
GTTAAATCAT CTCATAGTTT GGCAAAAAC TCTACCTCTG AAAAATGAAA AGAAAAA	180
AAACTCCATT CTGTGCTGGA CTCACACAGG CTAATAAAAA GCAGGACTGT ATTGCTTTGC	240
ACTGTAGCTG TCAAATTCTC AGCAATGAAA TACAGACCCT GACTCTCTCA GTCCCTTGCG	300
TCCTACCCCC TCAGACCACC AAAAAAGGAA TGGCGGGGGT GGGGGATGGG GTATCATTTA	360
TCCTCTCCCA TTCTAGAGGG AATCTTGTCT GTnGCTTTGT TTCACTTTTA ATTTCTTGGT	420
TTGAGGTCCA AACATCTCCT TTCCTGAATA AAGTTTCAC TGTGTTATA AACATACATA	480
TGCAAGGGGT GTTGGGAGCT GGTGCTCTGA AGATCTGTGC TTCTGCTGTC TTGTAGAGAT	540
ACCACACACT TGCCATCAGA GAAGAATGGA CATTGCAACA ATGAGAAAGA AAGAGAGGAA	600
GTAGAGAAGG GGGGAnAGAG GGAGGGAGGG AAGGAGGGAG GGAnG	645

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs

1034

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

```
CAGCCAGGTA AGCAGTAGTG CTTTTTGGTG TGTGGCAGTA AGATGAGTTA TTCTGGGATC      60
CCAGTTCTGG TTTGGAGTGA CAGGAGACCC TAGAGTTCCT GAAGCAGCTG GTCAATTTAG      120
CAGATGTTTG TACCTCAACC AATTTGAAAT GGATTTGGCA ATACAAGGTG AACAGTGTAG      180
TCACATGTCT TGTCTCTCCA TTGGGACATC ACAGGGTGCC CCCTAGGGAC CCGTTGAGCC      240
CTGGAGAGAA AGCTGGTGGT GATAGGGCTG ACCATGCAAG GGAGGGCTGG CAGGCACAGC      300
CGCCCTAGGG AAGGCAGGGA GAGGAGGCAC CTGTTCTGGG CCAGACATCC CACTGCTAGA      360
TCATCTCATC CATTCCGGAG CTGATTTGGC CCTATCCCCT GGAAGATGGA AGTACGCCTT      420
AGAGAGCGCA TGGCAGAGCC TGGATGTCCA TGCCAAGTCC AAATCTCAA TCGTTCACAG      480
ACTAGCTACA CGACACTGGG CGAGGGTGTC CTTCTCCGTG AAACCAGGAC AGTGAGACCC      540
TCCCTTGTA ACCATACAGC AGCCGTGGGG CTCGAAGGCC ACTGCTGTCA GAGCCAGTGC      600
CCTCCAGGGT GGC GACTCCT AGGGAAGGTC CCAGCCTCAG GCTGTGCCAA GTGCACCTGC      660
TTCTCACCTG CAAAATTGAC C                                          681
```

(2) INFORMATION FOR SEQ ID NO: 543:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 553 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

```
AGTAAATCTG TATTTGAAGG TGAGTCTGAA TTAACACTGT CTCCTTTTGA GGGCTTGATC      60
TCAGCAGTCA GATCAAGGGC TGTCTTGTA CTGCATCAGC AGACAAATAC GTGAAGATCT      120
GGGACATACT GGGAGACAGG CCGAGTCTGG TTCATTCCCG GGACATGAAA ATGGTAAGAA      180
TCTCCCTGAG TCTCTTAGTT TTCTGTTTTT CACCTGTGTC GCTTGTTCATT CTCGGGGAAT      240
CAGTGCAGTA AAGAATGTGG ACAAGTTGGG AAGTTAATTG TGGTGGGAGG TTTAGGGGCC      300
TCAGACCATT CTGGGAGAAG AGAGACTCGG AGGGTCAGTT TCTACTTCAC ACGAGTAACA      360
GCTGTCGAGT AAGGAGGGGG CGAGGGCTTC TCTAGGACAC AGGTGAAGTG GCCATTGTCT      420
```

1035

CACCCTAGGA AATCCTGATG CTTAGAAAGA ACCAGGAATT TTTCTGTATT GAACACCTGT 480
 TGTGTACCAG GCACTGAGCT TGATAGATCA CAGAACACCA CATAGCTGTT GAAAATCATG 540
 TACCTGTGTA T^{Tn} 553

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

CCTTTTCACA AAAAGCAGTC CTTATCACGG GGTGCGTATT CTTGTGCACC CCTGTGTCAT 60
 CCGCACATGA TGACCCAGCA GTTGGTACAT GGTAAGTATG ACCAATACAA TCTGCAAAGT 120
 GAGTCCGGGG TGATGCTGAG TCATAACCCCT CCAAAAAAAG CTGATCTCTG CAAATTGGAC 180
 CCTCGCTTAC CTGGAAGTAA TAATCTGGCT TTGCAAGGCT GCACAGCATA GTAAGTAACA 240
 ACCCTTGTAG CATTCGGTTC TCATATCAAT CAGACTGGAG GGTAAGATTG TCTACCTTGC 300
 TCGTCACTGG ATTCTTCTA AGGGCCTTGC AACAGATTG TCAGATGAAA GGGTGAGCGA 360
 GCAACCAGCA GAAAGGCACA GGATGGGATC ATTGTTAACA GCACCGACCT GGCGCTGGTT 420
 TTGTGGTGCA GTGGGTAAAG CCACCACCTG TAACACCGGC AACCCAGAGG AACACGGGTT 480
 CAAGTCCGAG CTGCTCCACT TCCAATCCAT CCCTATTAAT GTAGAGGATG GGGGTCCCAG 540
 CCATCCAA_nAA GAGAA 555

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

AACTCTGCCT TTCCAATAAA TAAATCTTTT TTTTTTTAAT TAAAACCCAG AAACCTGGCA 60
 CCCTCAGTGA TTGAGAAACT TTACCTGAAT GCTTTTTTGGC ACGTTCCTTC ATGATCCAAC 120
 CACCTGGACA AAACCCATTC TATGTGGTCT CAGGTGAGCT TGAAACTGTA ATGG_nAGAGA 180
 GGTCCACTAT GTGGCCTTTG TCAGTCCTCC TTTCTCTCCT CACCGCTCAT GTTTCAA_nAG 240

1036

ATAGATATCT ATTTCCAAGA TCTTTGGAGG AAACCATCAA GATCAGGGAA AACATAACAG	300
CAAAAGTTCT GTACCCCTCC TGGATGGTTT TCTCCCCAAC ACCATCCATG GGCAGAGAGGC	360
ACAGAAATGG TTCCCTACTG GTATTGGCCA TGGCTTCCTG GAAGCCATCT TGAAGGGGA	420
CTAGAACAAA CACATTTTTA GCCCCTCATA TCCAGCATCA AAAGGAAAAC CCAAGTAAAC	480
AATTAAATAA TCCTGGCATG GTGAGGATAT ACGGAGTCAC TTGGGTGAAC CTGGAGTGGA	540
CTATCTGTCT AGCT	554

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

ATCCTGAAGA ATAATTGATT TGTTAATAGA AGCACTCAAT GCCTCAATCC CTAAATCTAC	60
TATGTCAAGA CATATTTCCA AAGTTGATTT TGTGAAGGTC CTTACAGAAT ATGTAACATT	120
AGCTCTCCTC AGGTAGCCAT TTGGTTCTGC AACACACTCC TCAAAACCTA TTTTACTACT	180
GACTACTACT GCTGACATTC TCAACTCACA CAAATAGTTC AAAAAGCAGT GCTATGTAAA	240
ACTTTTCAAA AAGTGATTTA AATAGTTTCA TCACACTTCA TTTTGCCAAC CAGGTGAATG	300
AAGCAATTTT CCTCAAAGGA CTAAATTTT TAACAAAAGG TCAACTCTAG AATTCAGATA	360
TAGTGAGTTG AAGCATCAAC TTGCCTCCTG TAAACCACTT ATATTCTTAA TTTTCATTGT	420
TCTTTAAATT CTTTAGTTAT TTCCTTGAA AGGCAGATGG ACAGTGAGGG GTGCGGTAGG	480
GGTGGCAGGG AGGGAGTGGT TTCCAACATG TGCTCCATTC TGTAACGCT TACAACAACC	540
AGGGTTGGGC CAGGGT	556

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

AATCGTTGAT CAGATCGCGA ATAACGCTTC GGGAGATTTC TTCGCCGGA TAACTGAAA	60
-----------------------------------------------------------------	----

1037

TCCAGTGCTT TTTATTTCATG TGATACCCTG GCTTAATGCT TGGGTATATT TGCTGATTTA	120
ACAGGGATTT TTGTGGATCG GACTTCAGAT TGATAAAGGG GACGCCGCGT ACTCCGACGA	180
CAGCATAAAA ATCTTGCCGC CAATTTTAAA AACATCGAAC TCCGGGCCAA AAGGCCAGCA	240
AAGCTCGACA AAGGGTAACT CAAGGGCCAG GCGTTTCGCG TTTCGTGCAG TGATTGCTTA	300
TCCATAAAGC TTCCTTTAGG CGAAGGAGAA TAAGCAAAGT ATGCCGCGAA GTACGGCGAT	360
AATCGACGTT TAATCCGCCA GCGAGAACCA GCGTCGCCAG ATAAAGCGCA GAACAAAATA	420
CTCAATAGCG CCCAGCACTA AAAACCACAG ACAAACAAT AAAGTGTAAG GCTGACTAAG	480
ATCCATCAGA TGGAACATGG TCACCAAGTTT TTGTGCCAGC GCCAGCCCCA GTGCGGGGGC	540
GGGCAGCAGC AG	552

(2) INFORMATION FOR SEQ ID NO: 548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

GGGTGAGCGC TTTGTGGCCA CTACCCACAC TAACGCCTAC TTTTGATTTT AATGCCAGTT	60
TAATGTAGGG GTGAATCTCT TTCTTTGGGA TAATTCAAAA AATGCATTTA CCTGGCCCTT	120
GGGGTACGGC ATTTGGGACA TCAAATGCTC CACTGCGTAG TCTCTCTGCC CTCAGCGAAG	180
TCTTCATCGT TGTCTCAGTC ACAGTGCTCC TGTGGGCCCT CCGTGGTCCG CTGTCGGTGC	240
AATGCGCTGT AGTTTGGGGG AGGAGTCGTT GTGAATGGAA AGGAAGCGTT GGATGGGCAG	300
TCATGTACAG AAGGTGACTG TTGCAAGGAC AGCGTACTGG ACACATAACG ATGTGTGTGG	360
GCTTGGGCAG AACCAGGCCA GGCTGTTGAA GCAAGTAGAG TGGCCTATTT TCCCCTAAGG	420
GGCAACTGGG GGCCnAAnTG GTT	443

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

1038

AAAGCTCTAC ATCTAGCTAG TTGGTAAGAG TATTCTTTGG GACAGATGAT GGGCAAGATG	60
GAGATAGCAA GTATGAATCA GCACAAAAGT CTGGGTGCAC TTAGAAAAAT GAGCACAAAT	120
CACATATTTT GTTAATATTT TGTCAGTATC TTTTATTTA TATAAACAAT TGTTATAATG	180
AGTAAATCCA GTTCAACCAT TGACATTCTA TCTAAATATT TTCCAGGTTG CCTAACCCAC	240
AATTCTATTC CCATGGCAAA ATGTGTTTAC CCAACATTTC TGAGCATGCT TTGATTTTTTC	300
TGGGCCCTGC AATTTCTTTC ATTTGAAAAT CTCTTGCCC CCTTTAAATA TCCAATTTAT	360
TTATATGAAC TGTCTCTGAA GCCTTCCCCA ATAATCACAC TGGAGTGTGT CCCTAGACTT	420
CTACAATATT TTGTTTGAAG CAGTCATTCA ACATTTATGT GACATAATAT TCACTTAAG	480
TTGTGTGTGT AAATATTCAA ATTTCCCTAC CCTATTCAA TCTCTTGAAA AGTAAGGAGA	540
ATAGATTAA AATATTATAA AChTTATAGC TGCATAGCG	579

(2) INFORMATION FOR SEQ ID NO: 550:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

TGTATCGCTG TTCAGATCAG TGCCTCTGAG GGGACATGGT CTCTGCAGCT TCTCATTTGGT	60
CACTATCTGC TCCTGTCTCT TCAAGGGTGA TTTTAAATGC AGAGCAAGGT TATACAGCTT	120
CCATTTACAA TTTTACAGG GAATGCAATG AATCAAAAAG AAATAATCCA GAAGAGGAAA	180
ATCTGTATGG TTTTACATAG GCAATTAGAC CTTCTCCAAT TTTGTTTCAGC ATGCTTCAAA	240
TGGAAATCTT AGCAACAATT TCAAGTGGAA ATCTCAGCCG TGAACACTAA GTTCTTTTCA	300
CAAAAATAGA TACAGATTTT TCAAACATCA ATATGAAACA TTTTAAATA TAGAAATAAA	360
GTACTGAAAG TATTTAGAAA AAAACAAGCA AAATATTGCC TATTCAGTTA TAAATACAGT	420
GCCAGTTGTG ACCCTTTATG GTCTGGAGAA TTTTTCCT ATGGATAAAA TTGTAATATT	480
AGGACAGATT GTCAATTCAT CTGGTCCAAT CTGATTTATT TTCnTATTCh AAAAATTTAA	540
AACATTGTTT AAAATATATG ChACATATAA GGChAGACTA ATGGTATA	588

(2) INFORMATION FOR SEQ ID NO: 551:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 700 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

nAGAACGTAG GATACTGATT CGTTTCAGAC GGATGCGCGC ACAGGGAGCG TCTATGCACA	60
GCTTGTCGGT GCGCCGCGCG TTGCAGGATT GCTGCTGAAC ATAGATATTC CCTCTCTCCC	120
TGACGGGTAC TCTTTTATA CTGCAGCACA TATTCCCAGA TGCAATGCCG TTCGGTGTGG	180
GGAAAATACT GTGCCGTTT TTGCGCATGG AGAGGTGGTG TACGCAGGGG AACCGGTGGG	240
TATCCTCATT GGGCCTGATG AGCATGTGGT ACGTAATTTA GTGCAAGATG TGGTGGTGCA	300
TACGTGCGCA GAGCGGGCCT GTGCGTCGGA AATACTCTGT GGAATCAGTG AAGGGGAACC	360
CCTCGCTCAA AAGGTGGCGG TGCAAGGAGA TGCAGAACT GCTTTTAAAC GCGCATCACA	420
CACGGTATGC TCCTCTTGT CATTGTAGCC GCGTGACAC TACTTTGCGG AAATGCCAGA	480
AGTACAGGCA CTACCCGACG CGCACGGTCT GCACGTGTAC GCTGCTACGC ATGGCCTGCG	540
CACATGAGAA AAATATCGC GCAGGTACTG AATATTTCTG AGCATGCGGT GCACGTACAT	600
CCGCAGCAGG AAGCGCTTTC CTGTGATGGG AGAATATGGT TCCCCTCAGT GATGGCAAGT	660
CAGGCGGCGC TTGnAnCCTA TTGTGCGAAA AAGCCGGTAC	700

(2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

CACGTTGCAG GAAGAAGATC AGCTGCTTGC AAGCAGGTCA TCGTGCAGCG CAnATGTGGT	60
TTTCTGTACA CCACACGTGT TCTACCATGC ACTGTGCTCG AAATGGCGT GGTcAGGGAG	120
TATTTTTTCT CGCAGGGGAA GACGTCACGA TGATTGAGCA ACTTTCGGTG CGCAACGTTG	180
CGCTCATTCa ATCTTTGGCG TTGGAGTTTG GTGCACAGTT TACTGCCCTC TCAGGGGAGA	240
CGGGTGCGGG TAAGTCAATG ATACTCGGCG CGCTGTCCTT TCTCTGTGGG CAAAAGGTAG	300
GGCCTGATCT TATTGCAAG GATGAGAACG AGGCATGGGT TTCTGCGGTG TTTCGCTGTG	360
ATCACGCACC GCTGCGTGCA CACATGGTTG GCAGAACGGA GTATTGAGCC TGAGCACCAC	420
CGCGTGCTCC TTCGTCGGGT GATGCGGCGT ACCGGTCGTG GCACGGCGTG GATTCAAAAC	480

1040

GTCCCGGTCT CTCGCGCAAT TTGGAGTTT TCACGTCATT TTCATAGACC TCCACGGACA 540
GCATGAACAC CAATC 555

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

CAATCCATCT GAACACCTGC ACCCCACGAA AGCGCTCAGC AAACGCACAC ACCTTCTGGA 60
TTTCTTCTGG CAAAAGCCCC GAAAGGGCGC ACACCACTCC ATATACGCTC CACCCCCTCG 120
TCGCAAAGTC CTGCACCACC TCCGACGAAG AGGAGGACCC CGACCACCAC AAAAAAGCG 180
CCGAATCGAC AGGCATCGCG CAnCCACACC TGCGCAACGA GCCGTTTACA CTTGGCAAAC 240
GCCACCCATA CCCAAGCTTA CCAGGAAGAA AAAGGGGGGA AACTACGATG CACCCTCCAA 300
CTTCACTCAT AAGCTCAGAA ACAACACGGT TCTTAACCCC AAAGTCTGA AAGGGACGAA 360
TGTCTTCAAG CGCCTTTTGC TTCTGCCCCG GCTTGCGGTA GCAGTCTTGC AAGCTCCACA 420
TATACGCGAT AGTTTTTCCG ATTCAAGCTG CACGAGTCGA TTCAAGACTC ACAACCGGCT 480
TCTTCGTATC TCCCCTGGAG TTTACAAAGG ACTGCGAGCC CGAGCGTGGC ATAGGCATCG 540
TAATCGATAT CCAA 554

(2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

CAGCATGGTG CGnTGAATGT GTTCCCCGGG CnTTGTACAC ACCGCCCGTC ACACCATCCG 60
AAGTTGGAGA TACCCGAAGT CACTAGCCTA ACCCGCAAGG GAGGGCGGTG CCGAAGGTAT 120
GTTTGTAAG GAGGGTGAAG TCGTAACAAG GTAGCCGTAC CGGAAGGTGC GGCTGGATCA 180
CCTCCTTTCT AAGAGAAAGG GTATGGGCAT GGCATGGTGC CGTGTTCGnC GTGTGGCGGA 240
AGCCACACGG TAGGTTTTTC TGCTCctGCA CGGCAGTCTC TCCCCTTCCC TTTTGAAAAG 300

1041

GGGCTTGTAG CTCAGTTGGT TAGAGCACTT CTCTGATAAG GAAGGGGTCA TTAGTTCAAC	360
TCTAATCAAG CCCACTATTA TTCTTTATGT CCCTTTGTTT TGTTTATGGG GTAAGGAGTA	420
GGTGGTAGGT GATTTTTGAG AGTATTAGGG TGGGGTGTGA AGTTGAGAAG GGATGGATAA	480
TATGGTCAAG CGAATAGTGG TTTACGGTGG ATGTCTTGGA GTTGTCAGGC GATGAAGGTC	540
GTGATAAGCT GCGAAAAGCC TCGGGGAGGA GCACATGTCC TGTGATCCGG GGATGACCGA	600
ATGGGGTAAC CCGACAGGgT AAAgCCTTGT CATTCGCTTC CTGAATGAAT AGGGAGGGTA	660
AGGCGAAACT GGGTGAAGT ACCCATCTAA GTAACCTGGG AAAAGAAATC AAGAGAGATT	720
CCGAAAGTAG TGGCGAGCGA AATTGGAGGA GCCTAAACCT GTGTCTAACA GGGGTTGTAG	780
GGCCGCGCGG GCTTGCGTTC GGTGGGTGAA ATAATCCGGC CTATAGCAGA AAGGTTTTGG	840
GAAAGCCTGA CAGAGAGGGT GAAATCCCCG TATGCGGAAT GGGGCGGACC TGCTGGTGCG	900
GTACCTGAGT AACGGCGGGA CACGA	925

(2) INFORMATION FOR SEQ ID NO: 555:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 940 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

TCTGGGCTCG GACGGTACAG TAGGCGCGAA TAAAAATTCA ATTAAGATTA TTGGTGAGGC	60
GACGGATAAT AACGCGCAGG CTTACTTTGC CTACGATAGC AAGAAGTCTG GTGGTTTTAC	120
TATTTCTCAT TTGCGTTTTG GAAAGCAGAA GATCCGTAAG CCCTACCTCA TTACGCAGCG	180
GATTTTGTAG CGTGTCTATA GTTTACGTAC CTTGAAACCT TTGACATGCT CAAAACGCTC	240
AAGCGTGGAG GGACCTTTTT GCTGAATGCG CCGTACAGTG AGCATGAGGT GTGGCATCAC	300
ATACCCATAG AAGTCCAGCG TCAGATCATT GAAAAGGAGG TGAAGTTTTA CGTCATCGAT	360
GCGATTCTTA TCGCTCAGAA GCGGGGATG GGCACACGTA TCAATGTGGT GATGCAAACG	420
GCTTTTTcAA AATTTTTGGT ATCTgCCGGA AGCTGAGGCG ATTGACCTGA TTAAGAAATT	480
TATACAGAAG GCCTACGGCA AAAAGGgTGG GGAGGTTGTA CAGAGGAACA TCACCACTAT	540
CGATAtGGCG CTCGCTGGGG TGGGATTGGT GGAGTATCCG GGAGTTGCCG GTAGTTTGGT	600
GACGCGTCGT CCTGCGATGA GTTCCGATGC TCCGGAGTTT GTGCAAAGCG TGTTAGGTAC	660
TATTGCGCTC AATCAGGGGG ATAGTCTTGG GGTGAGCGCA CTACCAGAGG ATGGTACCTA	720

1042

TCCTACTGGT ACCACGCATA CGAGAAGCGC TGTATAGCCG AGACTATACC CATTGGGATC	780
CGTCTGTTTG TATCCATGTG GTCATGCGCT AGGTGTGTCC TCACGCATTA TCCGCATGAA	840
AGCGTACGAT GGTAAGGAGC TCGAGCAGCG CCTTCTAAGT TTGCTTCCTG TGGACTACAA	900
AGGCAAGGAA TTGGGGAAGC GAATTTACGA TTCAGTTTCC	940

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

ACAACCACTG CCACGATGCG CCCTGCCTTG TCCACAACAT AAGTAGTTGG CAGACCACGG	60
GAAGCAAAAA CACTCCCCAA ACTCCCCTCC TCGTCAAGAT AGATAGGAAA GGTATGCTTT	120
CCACGCGCGA TAAAACTTTC CACCTGTTTT CTCGAGTCAC CAACGTTGAC CGCGACAATC	180
TGAAAGTCAT TCCCCCTCAT AAGAGCCTGC ATGCGATCCA TAGACGGCAT CTCCGCACGA	240
CAGGGCGGAC ACCACGTAGC CAAAAGTTC AAAAGCGTCA CCTTTCCTT GAAAAGGCTA	300
GGAACCACTG CCTCCCCCTT CAGGCCTTCG CATGAAAGTC ACTAGAAAGG TCGAGCGGGT	360
TTGGGATACA CAAAAAAGC GAAACGCTCG AGCGCCTTTC AGCGAGCGGG AAGGTACATC	420
CGCATTGTGC GCCACATCGG CGGCTTGTAC GCnGGAAACA CCCCACACCG CAGCACCAGG	480
ACGGAAGGAA CACAAGGGGA CGCGCGTAA GCAnCGGTGC TACGGGAGCA ACTCATGCAC	540
AGGGAACATT CACT	554

(2) INFORMATION FOR SEQ ID NO: 557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

GCGTCAAGCA CCGGGAAGCG CACTACGCTC CAATATCTAT TAAAAGATTT TGTACCTCGT	60
CCCAGACAAA TGTGGGATAT AGCGTATGCA TACAATTTTG TGCATCCGCA CGnAACCGCA	120
GTGcTGCAG TTTCCGGCGG GAGAAGGGAT GCCTTTTGCT ACGGCGTTGA GGAGATCGGT	180

1043

TAACGCTATT CTCAATACAG CACAGGATAT TGTGAAAAGT GATGCCTTCT TACGTGAGCG 240
GCGCACATTG CTGGCTGATA TTGAAACACG TGAGnTGCTG AGCTTTCACG TATTGAAGCG 300
GAGTTGTATA CGCGTGGGTT TCGTGTGAGA TGGCATAGGA AACGTGGTAC GTACTCCTTT 360
GATTTAGTTC CCCTATTAAA GGGAAAAGAC AGTAGCTTTG AAGCGCTGCA CGATTTAGCT 420
TCCCGCGCGA AnTTTACTAG ATGTGTAGTA CACGAACTCC ATGCGCGATA TCGTCTTTCC 480
TGTGATGAGG TTTCTTCGCT GCTCCATACG TTGCGCACnG CGGGCGGGC CGCCGTAAGG 540
CGTCTTGCGC AnTACTACCG TCGCGGTTTG CGG 573

(2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

TGGGCTGCTC TACCGGAGAG AAAGAGATGG AAAAGGCTGC AGACATCATT CGCATGTACG 60
TTACCGACAC GCTTCTTCT GTGCGAACAT TTAGGCAGGA GTCACACACG CGCGCAACCT 120
ACGGCTTTTG CACAGAGGCT CACGGTACAG ATACCTCTTC AACGATAGAT TTTTCACAAC 180
TGGTGTTCAC CGCAGAACAG GTACGCACCA TTGAAATCGC GAAACTATT ACAAAAATTG 240
AAGATCGGGT ACTTGCGTAT GCAATCAAAT ACTGGCACAG ATACGATGAT CGAGCCTTTG 300
AGAACACCGT GCTACTGTAC AGCAGAAAGT ATAAACACA TCACTACAAT ATCTTCATTC 360
AATTAAAACT GGACGGGTCA CCAATGGAAA GACGAnGATA TTTTGCACTG GTGCTCGCGC 420
ACGTCGCCTC AGGTATACTA CAGCATCAGT GGTGATCTGT ATTGCAACGA AACGGCACGG 480
TTAAAAGCGC GCCGGTAGAA CGTGCGGAGC ATCCATCATC AAAAGGGTAA AA 532

(2) INFORMATION FOR SEQ ID NO: 559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

TTCAGATCAG AAGCAAGGAC AACAGGAAAA GCGTAGGCAC TGTGTTCCAA TTGCTCACAC 60

1044

CGGTGAAGCG TACCGTGACG CGTACGCAAA AGCGCAGAGG AGTATCGGTC GTAGATTGCG	120
CGCCTGAGGG CAATATTTTT TTCTTGCTGC TTTACTTGGA CACACGCGAG CGCCGCGTTT	180
CATATCCGGC AGCATATCAA CGGCAAGCGC TTCTGGCACA AGCGCCTGAA GCCGACGCGC	240
GCAAnGCGGCC TCAAAGGCCA TGAGTACCGC GCCGCCGCCT GCGGTAAGCA TATCGTGTGC	300
CTCCAATCCC ACGATGACAC ACGAGCCAAA GTTCCCACT TCTTTTCTCC CAATACTGCA	360
CCGACACTCT GGAGAGCTGT CTTCGATGAC GGGTATCCCC AGTTCCAAAA ACACCGCTGC	420
AAGAnGCACA TTTTCCAAGT GTTTCAGGCA CAAGAAGCGC ACGAGCGCCA AGCGCGAATG	480
CCATTTCCAC CACATCACGG GACAACAAAC CGCTGTGATG TCTAAGTCAA GGACAAn	537

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

TTTAnTTAnG GATCCCCCTC CGTTTCCGTC GCTGCCGTCG CCGAGGCCTG TGCACTCCCC	60
GGCCACCGAT TGGAGGCAAC CAAAAACGCT ACGGATAAAA CGCGCATGnT GACCTGCTTC	120
ACACGCGCCC GACTGCGCTG CCCCCGCTTC ACGTTCCCTTG AGCCTGACTC GTTCGCCTGG	180
GACACACCGC CTGGGCATGC CCGACTGTGT TCCCACCTGC ATAGCGCTGG ACTCTCGTTT	240
CCTCTCGTCG TAAAACCGAC AGACAACATG GGAGCCC GCGTGCACGCT CGCGCAATGC	300
AAGGATACCC TCATAATGC CTGCGCCGTG GCGGCCAGTT CTCTCGCAGC GGCCGGGTGA	360
TTATCGAGGA ATTTATTGTC GGAAGAGAGT TTTCCCTGGA AGGGCTnCAT ATTCGACGGG	420
ACGTTGTACG TCACCGCACT TGCCGATCGC CACATCTGCT TTCCTCCCTC ATTCGTAGAA	480
ATGGGACACA CGCTCCCGGG CAnGCGCTCT GTACACAAGA CAnACAAGCG CTCATTGAC	540
ACCTTCCACA ACGGTGTGCG GGCA	564

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

CAACTTTATC TTCTATCTTG CCACTCCCC TAGCCTGTAC GAAACTATCC CCACGCAGCT	60
TGCTATGCAC CACTTGAACC GGAACAGGG TAATTTTCGC AGGGTAGTTA TTGAAAAACC	120
CTTTGGCTAC AACCTAGAAA CCGCGCAnAC CTTAATGCGA GCTTGCCTGC CCACTTTCAG	180
GAAAACCAAA CCTATCGCAT CGATCACTAT CTGGGTAAGG AAACGGTCCA AAACATCCTG	240
GTCACGCT TTGCCAATCC CCTTTTCGAG CCCACATGGA ACCGGACCCA TATCGATTAC	300
GTTGAAATTA CTGCAAGCGA ATCACTAGGT GTCGAAAACC GCGGCGGTTA CTACGACCAG	360
TCCGGTGCAT TGCGCGATAT GATCCAAAAC CACTTGTTAC TCCTCTGGGT ATATCGCGAT	420
GGAGGCGCCC GCCGTCGTGA GTTCAAGTCG TCTACGGATG AAATCGTAAA AGTCTTGA	480
GCCTGCGCCC TATGGGGAGA ACGCGACGTC ATGCAGCATA CGGTGCCTGC CCAATACGTC	540
GCGGGCAAGA TACG	554

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

ACATTGTAGG TGTCAAGATA CAGACACACG GCGCTGACTC CCATTAGAAA GGCACGCCAT	60
GCAGACGCAC GCAGTTCTGT ATAGCCTGAC GTATCTGCTG CCCCAGATTC AACGCATCCG	120
TCTTCTTCTT CACTTCTTCG GTTATGTGTT GCTGGACACT CGCGAAAAAC GCCGTTATTT	180
CCGTTGCGAT CATCGGCACT AAATCTGCCA GATCCTGTTT CACCTCATCT TGCACGCTCA	240
CCATGGTCAG AATGCTGTTT TGCTTACGTG ATAGTTGCTG CTTAATGAGC GCTTCGCCTA	300
CCATTCTCGC AGTATCGCCT AGACTACCCC CGACCGCTTG CATGTTTGCA TTATTTTTTG	360
CCACAGCCGC TTGCACTTTC TGATTAATTT CAGTGACGAT TTGCGTCTGT ACCTGCTCAA	420
ACCCCTTCAC CACCTGCTCC GCATCGTACT GCAGCAAAAC CTGCCCCATC AGGGAAAATG	480
CAGGAAGTGC AGGAAGCGGC GGCAGGTTTC GCGGACTTCC CTGCGGGGTG TGAAGATTTT	540
GCACAACCTT ACCGGTAGGT TTAGCAGGAT TAGGCTGAAC TGCCTCTAGC GCGTTTATGT	600
ACGTATCCCC CGAGATTCCA GCGCGCTTCG AACTCCAGCC GTTACTGTCT GCGTCGCCTG	660
TTGCACTACC TGGGTTACCC AGGCTTCCTG TTTTGTGACTT TCTCCCTGGA AGAGGTTATT	720

1046

TGAGAGGGCG GTGAGTTCAC TCTGCGCCCT CTGTGTGCGA TTTTGAAAGT CCTGTGCACT 780
CTGGTGTGTTG TTACCGGCGT CGAGGGCGAA GaGAAGCGGA AGCCGGCGCC TGGTTCGAGG 840
GTGAGTCGGC CCCCTACATT CCACAGCAGT TTATCCTgTT CTGATTGTTT GCGTCCTTCT 900
GTGCACCGAT GAGGTATCCG TCTTCTAGCG TAACATTGCT GGCAAGCTCT ACCGTGCACA 960
GAGGGTGTCC TG 972

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

CAGGATGGAG AGGGGGCACG CCGCTTTGGT GCAAAGGGGC ACGATTGTGT TATACCGCTG 60
CCTCCGGGTT GTCTTTTAAG GGATGCGCAG ACTCATGAGG TTTTGACGA TTTTGGTCAT 120
GCCCATGAAG GTTGCGTGAC GCTCCTTTCG GGTGGAAGGG GTGGTTGGGG GAATTATCAT 180
TTCCGTGGCC CAGTGCAGCA GGCTCCGCAA CGCGCGCATT CTGGGCAGCC GGGGCAGGAA 240
CGTGTGGTGC ACGTTGAACT GCGTATTGTG GCAGACGTTG GCTTTGTGGG GCTCCCCAAC 300
GCGGGCAAAT CTTCTTTGCT GAATTTTTTTT ACCCACGCGC GGTGCGGnTn TGGCCCCTTA 360
TCCTTTCACT ACCCGGATTC CTTACTTGGG GGTGCTGCGT ACGGGGGAGG GCGCGACGTG 420
ATCCTGGGCA GATGTTCCCT GGGnTTCTCG AACGCGCCTC GCAGGGTGTC GGCTTTGGGG 480
TGCGCTTTCT CAAGCACTTG ACCCTGCTGT GCGGGGCTTG CATTTCTCAT TGATCTTGCA 540
GATGAGCGTG CGCTGCATAC ATACGAATTG CTTTGCAAGG AATTGTACGC TTTCTCCCCT 600
GTCTTTGAGA nAAAAGCGC 619

(2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

GACAGACATT ATGGAGGTAA TTTTGGTTC ACTTGCTGGA GTTTCGGAAG GAGTAGAAGG 60

1047

ATACACAGTG CATGGGTCAA TGGTGCAGCG AATGTCAAAA CCTCGTGTG ATTTTCAGAT	120
GAAAAGCGTC GGTACTCATG AGATTTTATG TTCAGGAACG GTTCCTCTG AATATTTTAA	180
CGAATGTTTA GGTACGCGTT TGCAGTCGCG CGTGTACCAC ACGGTGGGAG GTTTACTCCT	240
GGAACGTTTT GGACGTCTCC CTACGGTAGG GGATGAGTTG GTAATTGAAG GATTGCGTTT	300
TAAGATACGC CGTGTACTCG ATCGGTATGT TGTGTC TGCC CTCGTGGACA CTCGAGCATG	360
TAGTCAAGCG TTGGCTGACG CCTAAGTAAG TACACAGGAT GGGGGCCGTA CTTTGCGGnA	420
TCTGCAATTA AGTTGTATGT TGGATCGTGT TCTACAGGAA TGTGTGCGCA AAGGGTGAnA	480
GCAGAGTTGC TACnTGTTGA AGTGGGTTC CGTTTCAGGT GTATCGCGGT GTGGAAA	537

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

CACGTTTCGTA ACAATTGGAC TGGTAGTGCA TGAGCGCTTC CTCACCTTTA AAAGTACTGG	60
ACTATTTACG GCACCACAGG ATAGAGGGGC ATTGTAATGG GAAGGTGCTG CTCTGTGCAA	120
TGCTCACAAA AAGTGCATGT CTTGAAAAAG TGTACCAGAG CCACTACACT GGTGCGCGTG	180
GGTTCTGCTG TTTCTCCGAA AGTTTTAAAA GGCTTTCGCG ATCTTTTACC GGATGAAGAG	240
ATTGAGCGTG CATTGCTCGT AGAAAACTG ACGGTGGCTT TAAGACAAAT GGGTTTTGTA	300
CCTATCGATA CCCCCGCGTT GGAGTACACC GAGGTTTTGC TGCGCAAAAG TGAGGGTGAC	360
ACAGAGAAGC AGATGTTTCG CTGTGTTGATA AGGTGGAAGA GATGTGGCCC TCCGCTTTGA	420
TCTTACGGTG CCGCTTGCGC GTTCGTTGCA ACGCACTATG CGCGTTTGTA TTTCTTTTAA	480
GCGCTATC	488

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

1048

CCTTTGCCCT nTTGTTTGA ACCCATTTCC CAAGGCCGGG GAAACTTTn GGGGCCCGTT	60
TAACCCAGGG GGAACCAACC TTGGAACCCA ATTCCCAGGC CCCnGGAATT nGCCCCAACC	120
GGCCGGCTTT TnCAAAACCG TnCCAGGCC GGCCGnATTC CAGGGTTTTG CCTTGGAGGT	180
TCTTAATCCC CTTTGGATTA TTTTAAAGGT CGGATTACTT TCCAAAGGAC CAGGAAAGAA	240
ACTTTGCCCC CTTCTTTTGA AAAGCCGGTT GAGCAAATTA TTTGCACCGC CATGCTCGTC	300
AGGAGCGGGG ATGTACTCAG GAGTTTTGTA GCCCCAGTAC TATGCCACCT ACGCGCACGT	360
AGGCCTACCT GCGCTCGAAC CGATCTATGC GCGTACGGCG GAGCTTGAGT CTACTCTGCA	420
GGATTTACGC GCCAAGCGTG ACCAGCTCTT GGAAACATGC ACATTTGGTT CAATTCCTGA	480
AAGAGTTGGC CTCCAGGCGA AGAGCGCGGT TGTTACAGCG AGGATTTCGC TGCTCGAAGC	540
AAAAATTCAA AAGATTATTA CGCTCTGTAC CCCGGATGTC ATTGCGCATC CGGACGTCGA	600
GCGCATGTAT CACGCAGGCG AGCTTTCCTC CGCACTCAGT GCCGCGTACG CACGGCTCAT	660
ATCCGACCGC GCGGTTTACG CGAGCAACCT TCAACATAGC CAGGAGCTTA TGGATGAGCA	720
AGAAGCACTC GACGCGCGCC TGCGCCCTTG ACTGTGGTGC CAAGCCGCTG AAGCGCGTTG	780
CGGCGTTCAC AGCGCAGGTC AGTGAAC TGG ATGAGGATAT CAATGCGCTG TGGGCGCATC	840
GGTGCTGCAT ACGCAAGTTG TTTCTTTTACC GAGGAAGGAT TTGnTCAGCC TCCTTTaTCT	900
CAGAAGACAA GACCGACGGT GCCCGATGAA CTCAGCACGC TGTTGCGTAC CGTGGCAGAA	960
GCGCGGATGC gTAGGGCACG TGCAGGGTAT CAGGTAGAGT GCGCCAAGCT CCGTCAAAAG	1020
CTTCAGTCAG AGCAGCGTGT GTGCGAAasT TTTGCAGATC AATCGaGGAA TATCGACGGG	1080
GGATcAAAGA GTACGAGGCG ATGATCGAAT CGGCGCACAG AACGTTGCGT TAAGCAAAGC	1140
CACGGTAGCG CGTCTGGCGC AGTCATTAGA GGAGGCGTCA GAACGCCTTA CCCTATTCTGA	1200
AACATCGCCG GAACCTATTG TTCTCTCTTC GGAAGTTCTG TCTGTCCCCC AAGAGAAGGC	1260
GAGTGTGTAG GTGCTCATGA GATAGAGCTC TCCGTGTCTT CTAGACGGGn GGGGGGGGGG	1320
TGAGGTAGAA GTGAGAGGAG GGGGAGTGAG TGGGCAGGCA GGTGATGCAA GCGGGGGTAC	1380
TTGCGGGCAT GGTATGTGCT GCTTCTGGTT ATGCAGGCGT ACTCACTCCG CAGTCAGTGG	1440
CACAGCCCAG CTCCAGTGGG GCATTGCGTT CCAGAAGAAT CCACGCACTG GCCCGGGCAA	1500
GCACACCCAT GGGTTTCGCA CTACCAATAG TCTGACTATT T	1541

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

CTGTGCTGCG CACCGTGCCA GCTGAGCGTC ATACCCGGAT CATTTT TAGA GAAC TGCTTC	60
TAGGACTGGT GCTCATGCTC TCCTTCCTTT TTTGCGGAAA AGTTTTCCTA TCTTTGTTCC	120
AGCTAGAAAC GGGAGTAATG AAAATGGCCG GAAGCGTCAT TCTCTTTCTC GTTGGCATCA	180
AGATGGTATT TCCTGATCAA CACGCGCTCC CCTCCACCAC AGAAGAGGAA CCGTTTATTG	240
TTCCCATCGC CACTCCCATG ATCGCnGTCC TTCGGCGTTC ACCACGCTGG TAATTATGGG	300
AGAGACGAnG GGACATCCCG TCTCGCCACC TGTGCTGCGC TGCTTGTTGC GTGGACGCTC	360
GCGTGCTCTTA TTATGATAAG CGCACCGTGT CTATACCGTC TTCTTAAAGA AAAGGGAATT	420
ACCGCGCTGA GCGAATCAn GTATnTGCTG CTCATTCTTC CATCCAGA	468

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

CCTGACATGG TGCACGGATC TGGAAGAGGC GCTCTATCAT TGTGGGGCGC TTA CTGGAGA	60
ATGCACAGCG AAGATATCCT AGATGCGCTG TTTGAGAAGC TCTGTGTGGG AAAGTGACCT	120
GCAGTACGGG AGATACGGGC GCGTGTGACT GATTAGTTAT ATTTCTTGGG GATGCAGCGT	180
CAGGTAAC TT TTTTCGGTAG AAAGGTGGAG GCGCGCGCCG TnCTGAGTCT ATGTGCACGC	240
ACGATCCTGC GCGCAACGTT CCGTGAATCA TGCGCACGCA AGCTCATTTT CAATTTCTTG	300
CTGCAATACG CGGCGCAGGG GCGTGCGCCC AAGAATGGGT CAAAGCCGTG TTCAAGACAG	360
TAGGCCTTTG CAGCCGCGCT GTAGCCAGCA CAATATCTTA CCGCGTAAGG TTCTGCGAGC	420
TCTCATTCGC ATCTAAAATT CCTGCAGGTC TCTCGCTCAA nGGAGCAAAC ATACGCATCG	480
TCAAAGCGAT TGAGAACTC CGAGAGA	507

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1050

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

TGCACAAnGA TGC GCGGTAA CACCGCATGC GATTGAGCAG GTGTGGAACG ACACATCACC	60
GTGCAGTACG CCTTTGGnTT GGTACAGGAT GCAACGCATG TGTTTTTTTT GTACGCGCAT	120
GAGCCCATGC GnGATCCGGC TTTTATTTTC TTTTCTGGAG TTGCTTGTGG GCGTGGTATG	180
CACGTGCTGC TCTTGGCTAC AACAAACGGAG GTCAGGGATA TCCATGTATT TCGCGACTTG	240
GTCTTTTTTAC TTGAGGAGGA GACGTTTGAG GATTTCTTTC GTGTCGAGCA CGAGAGATTT	300
GTAAGGCAGA AAAAGAAGCG TGTCGCACGC ACTGCGCTGT TAGAGCGCGG TTATCCATGT	360
TTTGAAGAAA ATTCATCGCG ACATCATGGA TGGGAATATT GATATGTCAA CTCTTTTGGA	420
GCAGGATTAG CGCTGCTTGA AAGACGCACG CCGTACCCTG TGTTGTCTTG GCAGTGC GGG	480
AGGTCAGGAT GAGAGGCAGC GC	502

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

GACGAATGCG ATGCCGACGG GTGATGTAAA TGCGATAAAG CCGGCTTATC TTAAGCAGTT	60
GCAGGATATT GCGTGGAAC TGGAGGATCA CAGCCGAGAG ATTCGGGAGG TTCGCTTTAC	120
TATCGAGGCG GGCAGTTTAT GGCTTATTGA GCAAAAACCT GTCGAAGCGA AGAGCACAAT	180
CTCTTTGGTA CGGTTGCTGC TCGACCTGTA CGAGCGCGAG GTGGTGGATG CTGAATACGT	240
GGTCAAGTCG GTAAAACCGG GTCAGCTGAA CGAGATTTTG CACCCGGTCA TTGATATGAC	300
GAGTGTGACA GGTTTGAAAT CCTCGCAGGG GGGATTATTG GTGTTCTTGG TGCGGCGGTT	360
GGGCGAGTGT ACTTTACCGn CTGATTCCCT CATGCGAGGA CGTGGACGTG TGGACGAAGA	420
TGGGCGGACA AGATACACGG TGTATCTTGT GnTATGCCTG CAACGnACGC GGGGGAnGTT	480
AAGGGCAATT GAGGTGGCAA CTGGTGTCTT TTCTAACGAG GGGGGGTACT	530

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs

1051

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

```
nTCTTTTnG CATACGGGGC ACGGGGACTC TGTGTGCCAT GTCCGTTTTT TGTCTACTTC      60
TTTCCTTTGG AAGGCGCTGT GTGGCGGCGG ATAATTTCTT TTCTTTCCTT GTGTGGAATC      120
TGGTTCTTGC CTTTCATCCCC TGGCTCATCT CGGCTATCTT GCACGTGCnC nGGGGGGGGG      180
TCCGGGGGGG GGGGnGTTCC TTATGCTGCT CTGGCTATTG TTTTTCCTCA ACGCTCCGTA      240
CATCCTTACC GATATTATCC ACTTGGGAAA GGGTAAGTCA TTTTGTCTT ACTATGACCT      300
TATTATTTTA CTCGCCTATA GTTTCACTGG TTTGTCTTAC GCGTTTGTCA GCCTTCACCT      360
TATTGAAAGC ATATTAGCCC GTGATTTTCA TATCAAAGG CCATCATAAT TTCAGTATTT      420
GAATTGTATC TCTGTGCATC GGTATATATC TGGGGCGTTC TGCCTGGAA TTCCGGGACA      480
TGTCTACAG GACGCACTAA TCTTCTGAA TnTGGTATCC G                          521
```

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

```
AGAAGTGGTC CTGCAACTTT ATCCGCCTCC ATCCAGTCTA TTAATTGTTG CCGGGAAGCT      60
AGAGTAAGCT TGCTGCACAC GAGGGGCGCA AGGCGGCGTG CGCACC GCCT ATTCCCTGGG      120
AGCAGCTCAT GTGCCAGATG CGTGCACAAT CCCGCGCGCA CACCGTCGGC GAGCTCTTCT      180
CTCCGTGGAA ATCGTAATGT TCATTGTGTT CGAGAGAAAT AACAAACCCG CAGTCTATGA      240
GGGGGTGCCG TACTCAGCAG GATTTTGGTA TATGTGCTCA AGCGCGATCT GTGCTTGTGC      300
AAACAGCATG ATACTTTCTG TCGCAGTCTG ATAACGCTTC TCAGCAACGA CACGCACAAT      360
GCCGCAGTTA ATGATGAGCA TTGCACAGGT GCGGCACGGT GTCATGGTAC AGTAGAGTGT      420
TGCGCCCTCT AGACCGATGC CCAAACGCGC TGCTGGCAA GGGCGTTTTG CTCTGCGTGC      480
ACGGTGCGAA CGCAATGCTG CGTGCACGTC CCGTCTTCAT                          520
```

(2) INFORMATION FOR SEQ ID NO: 573:

1052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

```
GCGGGTTTAT TAGAGTTGAT TGTGCAGGAA ACGCATACGA TTCATATTAG AATTTTCGAGT      60
TTGTACCCAG AAAGCGTAAC ATCTGCTTTT TTGCGTGCTA TTGCGCACAC GCGCGTGTCTG      120
CCTCATTTTC ATTTATCGGT TCAGTCGGGC AGTGATCGCG TGTACGACG CATGCGACGC      180
GCTTACACAC GTGCGGACAT TTATCAGGCA GTTCCGATT TACGGAGTGT GCGTGAAGAA      240
CCCTTTTGGG TTGTGACATA ATCGTCGGCT TTCCAGGGGA AACAGAGGAA GATTTTGCAG      300
ACACCCAGCG TATGTGCAA ACTTTGCGTT TTGAGGTAT CAGTATTCCG TTTCTGCACG      360
CCCCGGTACA GAAGCGTTGC TATGGATGCA AAATGCCTCA GCGTATTGCA GGAGAACGCG      420
TGCTGCATGC ACAACTGGCA GAGAAAACT AACGTGCCGT ATTGGAATAT GGAAGGGAG      480
GAACTAGTGC GGTGGTAAaA CATCCGTCGC ACGTGnTTTG ACAGAAAATT AAT      533
```

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

```
TCATTAGGCA CCCCAGGCTT TACACTTTAT GCTTCCGGCT CGTATGTTGT GTGGAATTGT      60
GAGCGGATAA CAATTTTACA CAGGCAATAT TCCCATCTTT CGTTACATGC GCAGTAAAAA      120
AGAGAACAGA GTCCCGTTCC TTTACCCACG CTATCAACTC ATTTGCGCAA TATTTTCAGCT      180
GATTGATAGT CATAGGAATG GCACCTGCTT CGGGGGAAAA AACTGTCTGA ATCGAATCAA      240
CAATAACGAA GGTAGGGCAT CGTGTATTTA AAACACGCTC GACATCCTCG ACCCGCGTCG      300
CACAAAGCAA CTCGATGTTT TGAATTGGAA TATTCAGCCG ATCCGCACGC CCACGAATTT      360
GCCCCGGAGA TTCTTCACCC GAAACATAGA GAACCGATTT CCCGCAGCTG CAGCGATTTG      420
TAACAGTAAT GTAGATTTAC CAATGCCCGG TTCCCCGCCA ATCATGATCG CGGAGTCTTT      480
ACGGCGCCTC CGCCGAGGAC ACGATCGAAC TCTGCGATAC CACAATAAT ACGCTGCGCA      540
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1053

TCCTGCGCGC GCACAGCACA CA

562

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

GTGCAACTTT ATCCGCTCC ATCCAGTCTA TTAATTAAAT CTATCGTTGA AGAGGTATCT	60
GTACCGTGAG CCTCTGTGCA AAAGCCGTAG TTGCGCGCGT GTGTGACTCC TGCCTAAATG	120
TTCGCACAGA AGAAAGCGTG TCGGTAACGT ACATGCGAAT GATGTCTGCA GCCTTTTCCA	180
TCTCTTTCTC TCGGTAGAGC AGCCATTGTG CATAATGCGT GTGCTTTCTG GAGAAATGAA	240
CGGACTCAAA GCGGTTGAGA GAAATAGAAC GCACAATCTT TTCGCAAACT CGGATCAGCG	300
TGCGCACGTC GGTCAAGTCG AGGGGCGCAA CCGCGGCGGC GAAAAAATCA ATAATTTTCT	360
TTATTTCTTG GATTTTCTTC TGAGCGAGCT CTGCTAGGGC ATCGGCAAGC ACTTCCTTAA	420
ACCGCACGTC CCTTTTGCGA TAATAGGACA TGAGGAGTAC CCTACGCTCC TTCTGAG	477

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

TTCTTTAGCA CCTCCAGCGC TTAGCCTGAA AATATGAAAC AGGTCTGTGC ACCGCACCAC	60
TTGCGAGAGT CCTGGGTGAG AGTGAGGAGC AGGGnCCCGn AGGGGGGGGG AGGAGGACAG	120
AGCAGCCTGA GCAGCACTGC CTGCAGAAAC CCACAGGCTG CAGCAAAGGC CAATACAAGG	180
TTTACTCAGG GCCACATCTG AGCAGCCCAG GGCCAGGCTC CCCAGATGGC CACAGCGGCC	240
AGGCcTGGnC CAGGCCAAAG CCAGGAGCCA GGAGCTGCAT CTGGGTCTCC CACGTGGGTG	300
ACAGGGGCCC ATAGACTTAG GCCATCTTCC CTTACTTTCC AAGGTGCATT AGCAGGGAGC	360
TGGATCAGAA GTGGAGCAGC CAGGACTCGA ACTGGCGCCC ATATGGGATG CCGGCACTGC	420
AGGGTGCCCT GGAGAGCTGC ATCTGAaCGC CCTCACACAG GGCTCCGCAG GGGTTTCTCT	480

1054

CGAATGCTTT GCCGGGTTTA TGGGGATGTG TTTGTTCTCA CTGCCAGTnG GAnCCTGAGA 540
TCCCCGGCCT GCTGTGCAGG AGCTCCTGC 569

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

TGTTTTCTCA GGTTCCTAAA GCTTCTTCCT AGAAAACCTCG AATGTGTGGA GGATTTGACT 60
CCAGGTGGAA CCAATTAGCG TTTGGCAGCT AAAAACAAAA ACTTACATGC TAAAATGCAT 120
TCAAAACCGT AAAGTCCATA GAGAATGTCC AGAAAACACA AACACAGAGG CAGTAGCAAG 180
ATCTGGGATT GAGATAGCCA CAACACACCA GATAGTTTTG TTTTCATTAA GGAGTATCTG 240
GACAAATTGT TGTAGTTTTG AAGTGAAATT TAACCAAAAA ATCACCGTGA AAGTGGTTTT 300
GGAGAAAAGC ACAATCTTGC TGTTCAAGCA ATGCATCCAA TGTCATGTTT CCAAATACAA 360
ATATCATGTT TTCTCAGGTT TCTGGAGCTT TCTTCCTGGA AAACCTCGAAT GTGTGGATTA 420
TTGACTCCA GGTGGAACGA ATTAGCGTTT GGCAGCTAAA AACAAAAACT TACAGCTAAA 480
ATGCATTCAA AACCGTAAAG TCCATAGAGA ATGTCCAGAA AACACAAACA AACACAGAGG 540
CTGTAGCAAG ATCTGGGGAT GAGATAGCCA CAACACACCA GATAGTTTTG TTTTCATCCA 600
GG 602

(2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

GTGTTTTCTG GACATTCTCT ATGGACTTTA CGGTTTTGAA TGCACTTTAG CATGTAAGTT 60
TTTGTATTCA GCTGGCAAAC GCCAATTGGT TCCACCTGGA GTCAAATCCT CCACACATTC 120
GTGTTTTCTA GAAAGAAGCT TTAGAAACCT GAGAAAACAT GATATTTCTT TCTGTAAACA 180
TGACATTGGA TGCATTTGCT GAACAGGAAG ATTGTGCTTT TCCCCAAAAT CACTTTCCT 240

1055

GTGATTTTTT GGGTTAATTT TACTTCAAAA CTACAACAAT TTGTCCAGAT ACTCCTGGAT 300
 GAAAACAAAA CTATCTGGTG TGTGTGGTT ACCTCATTCC CAGATCTTGC TACAGCCTCT 360
 GTGTTTGTGT TTTCTGGACA TTCTCTATGG ACTTTACGGT TTTGAATGCA TTTTAGCTGT 420
 AAGTTTTTGT TTTTAGCTGC CAAACGCTAA TTCGTTCCAC CTGGAGTCAA ATAATCCACA 480
 CATTCAAGTT TTCTAGAAAG AAAGCTCCAG AAACCTGAGA AAACATGATA TTTGTnTTTG 540
 GAAACATGAC ATTGGGATGC ATTTGCTGAA CAGCAAGATT GTGCTn 587

(2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

CGCGCTTGCA GTTCAGGCTC AGTTGCGCT GATTTTCTCT ATCACCACAG ACATAAAGGC 60
 CCAAGAAGAA GTGATCAGCC AGTCGATGGT AGAACAGACG AAAGACAGTG TGCACGTGTT 120
 GCACGCTATA CAGCACATCA CCGAGATCAC GCGCACGTTG CAGGAAAATT CGGGCGCCAT 180
 CTTGGACAAC AGCAAGCACG TAGAGGAGgG CGATGCTAGC CCTTTCGCGC ATCACGTCTG 240
 AAATCGACAG CAGCGTGTCG TCCATGCACA AAAACTCAGA ACAGGTAAA AAGTATGCTT 300
 CCTCAATCAC TGAAATCGGA CAGAAGAACA AGGATTCCAT AACGGACCTA GTCACTGAAT 360
 TGAGTAACAT GCGACTCTAG AGTCGCGGGG GCGCCTGTTA CCCTTCAGCT GCCATGCGTC 420
 TGCGCACTTC GTGcaGGTTA GCGGTGTGTC CTTTCGCGTA GAAAGGTGCG GCAtACGAGC 480
 AGGCAGTCCT CCACCACGGC GTTGCCTGT TCAACAAAGA TCCCCACCT AATCCCCCTC 540
 TTCTCTGCAA AGGCGTACTG TTGGCTCAAc TTCCGCGGAT CAGGGAAGAC TTCCGTCGCC 600
 ACCTGCACTG CAAAGTATGA ACACAGCTTT TGGTACACAT CCATGAGCGC ACTAnCCTGA 660
 CAGAAAGATA AGCGCCTGCA CAAAACAAAC GTGCTCTCGG GAC 703

(2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

AGTCAnTTCA ACGTGTTCGG CCGTGGCATA CAGCTCCCTG GTCTTCCTGA TTATCGCCCT	60
CGTGCGCAGG TTTTCGCACAG GCCGGAGAAG ACAGGCTCCG GCGTACGCAC GATAGGCGTT	120
TTGATAAGTG CGCGCAGTGC ACCACCGCCT GAAACGACAA TGAGCTTCCG TGAGCGTCTT	180
CGTATAGGTA CCGTTGAACG GAACGAACGA ACCGCCCCGAG AAGCTCTATG TCGGGCGTCT	240
CAGGCGCAAC GATGGAACCT CCAAGTGACA GAACGGTGAC CATGAAACCC TCTCGCCGGC	300
ATCGTAACGC AAAGAGACCC TTTGGATCCA GGCCCTGTGT GTATCTGGCA TTGCGTCCCA	360
GCGTGCACGG GCGCATGGAG TGTTCACAC GGGCGACACA GACTCCTAGT TCTTGATTTC	420
TGTGCAAAAA CCG	433

(2) INFORMATION FOR SEQ ID NO: 581:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

GATACGCAGC TTGCGACGGT GAGCTACCGC ACGTACACCG TACCTAAGGG AnCATACTAT	60
TAGTGCCATT GCGCTGCGCC AGGTACTCAA GCATATGGGG ACGCTGCTGT CGGTGAACGG	120
AATTTCAAAC GCGCGCAGAC TATCGGTAGG GGATCAAATT ACTATTCCGT CCATGGATGG	180
ACTCATGCAC ACGGTACAAA AGGGGCAGTC GCTTAnTGCA ATTGCCAGTC TCTTTCGTTT	240
GCCCCTGAAT ACGTTGCTGG ATGCGAATGA TTTAGTCAnT CGTGCAATTA CAntTTGGACA	300
GCGnTTGTTT ATTCCGGGTG CAAAATTATC TGCTTCnGAT TnAnGAAGG TGTTGGGGGA	360
GTTATTCATG TATCCAATTC GCGGGCGGCG CACCTCTGGG TTTnGGTACC GCTCAGATCC	420
CTTTTCAGGC AAnAGGAGCT TTCACAATGG GA	452

(2) INFORMATION FOR SEQ ID NO: 582:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

1057

CGCGATCCGC	ACGnCAngG	GGCAGAAGCC	TGCACTGGTG	GTGTCGGTGC	GCGATTGCTC	60
GGTGGTGA	TCTGGTGC	ACGAGCGTTT	CTTTGAGCGT	GACGGGGTAC	GCTACCATCA	120
TATCATCGAT	CCGGTTACCG	GGTTTCCGGC	ACACACTGAT	GTGGATTCTG	TGTCTATCTT	180
TnCACCCCGT	TCCACAGATG	CAGATGCGCT	TGCTACCGCC	TGTTTTGTAT	TGGGGTATGA	240
GAAAAGCTGT	GCGCTCTTGC	GTGAATTTCC	CGGTGTTGAC	GCGCTGTTTA	TTTTTCCTGA	300
CAAGCGCGTG	CGCGCAAGTG	CAGGGATTGT	CGATCGCGTG	CGTGTGCTCG	ATGCACGTTT	360
CGTGTTAGAG	CGTTAGGACA	GCACGTGTGC	TGTTCTGTGTG	TAAAAAATGT	GGCGGATGTC	420
CTCATCAGGT	GT					432

(2) INFORMATION FOR SEQ ID NO: 583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

CTGTGCTTAT	CAGCACGCCA	ACTAAAAGTC	CAACGATGAC	GCACGTACGA	CACTTGACTT	60
CTCGTGCGTA	GTGAAAAAGA	AGCGCGCCGT	ACATGCATGG	CAGCGCGGTA	AAAATCCAGC	120
GTAACGGCAC	TCCCCACACA	GCTTCTTCTT	TGCGAAAAAC	TGCGACGATA	TTCGGTCCAG	180
ACGCAAAAAA	GCAAGCGCTG	AGCACTGCCA	CCGTACAGAT	CGCAGAGAGG	AAGGAAAGAA	240
CGCGGTGCAT	CGGTCTGTCC	ACGTGCGCAG	AGAACAGGGT	GACACTCAAG	TGTTTACGTT	300
CACGCGCAGT	AAAATGCCTG	CAACACAGGA	AAACACGAAG	CTAACTGTGC	AACCGCGGCG	360
TTCAnAnGAG	GAGAAAAAAA	GGAAATGAAT	CTnCGTGCGC	GGAGAAAACC	TCGGAACCTA	420
CGCCCCGCTA	AGAAA					435

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

TGCAACACAC	CCCGAGCACG	CTCGGCGTTG	AGCTTACTTG	AGAGCGnnGG	CGTTGCACCC	60
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1058

AGAAAAGGAC AGAAGGAGCA GCAGGCTGCG TGGACGCACC GCGCACGCGC GCATCCCGCT	120
GTGCAACAAG CGGAGCACGG GTACGAGTAG CGGGAGGCGA CTTGGCAGAC GCTCGGTCAC	180
TCCGTGCATG CTTTGACGCA CCCTTTGACT CTGCAGATTC CCGAGTGTCA GAGGCAGGAG	240
AAGTTTTCCT GTCCTGCGCC GCGTCTGTGC GCTCAGCACG CGCCGGAGGA GAAACATCAA	300
GA nTTTTCGC ACGAGCGGTA GGGAC nTCCT TTACCACCGT GAG nTCAGGA nTTGCCCTCT	360
GTGTTGGCGC AGGAGT nTTC CCCAGCTCAG GA nTTTTTTC AGG nTTTTTA GCCATAAGCT	420
CGG nTCCATG ACGG	434

(2) INFORMATION FOR SEQ ID NO: 585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

TCTCTCATAC TGCTC nTACT CCTCTCTCAT CATTGTCTCT CCCCCTGTGA CATCCGCGCG	60
GTG nCCGCAC TGCCAGACAC CCTTCCTCCT GTGAGGCTGG TAATCGGCGT TGGAATAAAA	120
GGGCAGGGTA TCGCCTGCTT GCATTCTGCC GCCCTTCCTG AGAAGAAGGC GCGCATCGGC	180
AGTTCACTGA CTACCCTTCC GGCAGCCTCC GGTGCATCGT GCCTCACCTT TTTTACCCGT	240
GGACACATAC CCCAATTGCG CATTTCAAAA AGTCCGTTGA ACAATCGTTC GTCGTTTTCT	300
TACACGCAGA TGTGCAACAA CTACGAACGC AAAACATCAC GTGGCTTGGA TCCATTGCGC	360
GGACCGACCA CCCCCCTTGC TTCCATTCTT CGATTAGGCG CGCGGCGGAT TGTAGCCTAT	420
CTCAATT	427

(2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

CGGTAACACG TGGTTTGCGG CGCAGGCATT GGAGTAATTC ATCGTACAGG AAGTCCGGTT	60
TTGCCCAAT TTTTTC AATG AGCGGAGAGA TAATCCCGTC TTTCTGGGAA AGTAGGGCGT	120

1059

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GGAGTAGATG TTCCTCCTCA ACTTGACCGT GGTCTCCGC TTCTGCCAGA GATATGGCGT      180
CATTGAGCGC TTCGCTTGCT TTGACTGTGT ACCTGTCTGT GTTCATGGCG TGATTATAGG      240
TCTTTTGAAC GCTTTTTTCT CGTCATCGGT ATGTTTTTTC TACCGCTTGC AGGGGACTTA      300
CGGGAGTAGT CGCGGTGGAG AACAGGGGTG TACATGGTAT GCGGTGCGCT TTGGCAGGCC      360
GCGTAAGGCG TACCTnTAT ATTTTCTGTT TTGAATAGGC TCCGCGATTG GGAGTTGGGA      420
ATAGGAAAAA                                     430

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(2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

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GnCCCCATCA GGGAAAATGC AGGAAGTGCA GGAAGCGCG GCAGGTTCCG CGGACTTCCC      60
TGCGGGGnTG TGAAGATTTT GCACAACCTT ACCGGTAGTT TAGCAGGATT AGGCTGAACT      120
GCCTCTAGCG CGTTTATGTA CGTATCCCCC GAGATTCCAG CGCGCTTCGA ACTCCAGCCG      180
TTACTGTCTG CGTCGCCTGT TGCACTACCT GGGTTACCCA GGCTTCCTGT TTTTGACTTT      240
CTCCCTGGAA AGGTTATTTG AAAAGGGCGG TGAGTTCAC CTGCGCCCTC TGTGTGCGAT      300
TTTGAAAGTC CTGTGCACTC TGGTGTGGT TACCGGCGTC GAAGGGCGAA AGGAGAAAGC      360
GGAAACCGGG CGCCTGGTTT CCGAGGGTGA AGTCGGCCCC CTAACATTCC ACAGCAGTTT      420
AATCTnGGCG nGCGTTGTT                                     439

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(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

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TTCACCATCG AGGTGGAGCG CTCCTTGCGC GTTTTAGACG GTGCCGTCCT CGTACTCTGT      60
TCGGTTGCAG GCGTCCAGTC CCAGTCCATC ACTGTGACC GGCAGCTCCG CCGCTATCAC      120
GTGCCCCGTA TCTCATTTAT CAATAAGTGT GATCGTACGG GTGCCAACCC TTTCAAGGGA      180

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1060

GnACTTGTGG CGACAGCGCG TGCAGCAACG TGAAAAACAG CGCTCGTAAG CTCCCCTGCG	240
ATCTTATACA TATTCGGGAT CATAAGCAGC AATCCCTGAG AAGCAGTAAA AGTAGAAGAG	300
AGCGCCCCCG TCGTCAGTGC GCCATGAACA GCTCCCGAAG CGCCTGCCTC AGACTGAAGT	360
TCTACAACGG TGGGAACGGT ACCCCAGATA TTTGTGCGCC CCCGTGCGGA ATATTCGTCT	420
GCGATTTCTC CCATAGGACT GGAGGGAGTG ATAGGGAAGA TAGCAATGAC CTCACTAAGC	480
GCGTGAGCAA CGTGCCCCAn TCGGGTGTTA CCATCCATCA TGACGAGGTT CTTCTCAGAC	540
ATACGAnCGT CCTCTCTC	558

(2) INFORMATION FOR SEQ ID NO: 589:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

TAATTCCCGA ACAACnGTGC CAATCGTACT CCGCAATATT CACCGACAGC AACGCTGTCC	60
CCTTCTTnCC ATTGCTTCTA GTAAGCCCTT AAGCCAGGG GAGAATCTCG CGCTGGTAAT	120
CGTGCAGGGC TTTTCCCTTA ATTCTCAGGC CATGATCCAA ATCAGCGATG TCCGAGAGAG	180
TAAAGCAGTG ATAAAGACTT TTCAAGAGAG CAGAAAAGTC ACTGACCATA GCGTAnTCTC	240
TGCAAGATTA CCGCTATGCA TGTTTACTGC GATTTCCTGT AACGCAGCTG TGCGTGCAAG	300
GAGAGTGGTA CTAATCTCAC GCAAGAGTGC ACGCACTCTC CCCCTGAAAG AGTGGTAAGA	360
TTAAGGGTGA CGTCGGTATC CAAGGATTGG CA	392

(2) INFORMATION FOR SEQ ID NO: 590:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 507 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

CCGATAnCAT TACCTGGGAG GGGGATGCAC GCATTGTGCA GGCAGCGCGT GTTCTTACG	60
GTGCGGGGAC TAGGACTGCG CGTGACGATG CGGCGCTTAT CGATTTTCTT TTACGCAATA	120
AGCATACGTC TCCTTTTGAG CAGGTGGTCC TTACCTTCCA TGTACGTGCA CCGATTTTTC	180

1061

TCGCGCGTCA GTGGATGCGG CATCGCACTG CTCGCATCAG TGAGGTGTCT AGTCGTTATT	240
CGCTTCTTAG TCATGACTGT TATGTTCCGC AGAAACTTCA GTTGCAGTTC AGTCCACGCG	300
TAACAAGCAG GGCCGCGCGT CCGAAGTATC TCTCCTGAAC AGCAGCAGGA AGTGCGGGCA	360
GCGTTTGAAG CTCAGCAGAA AGCGGCGTGT GCnCTTTACG ACGCATTGAT CAAAAGAACA	420
nCGCGCGGGA GCTAGCGCGT ATTAACGTGC CGCTTTCGCT TACACCGAGT GGTATTGGCA	480
GATTGATTAC ACAATCTTTT CATTTTTT	507

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

TCCACCTGGA GTCTATACGC CACACATTCC GTTTTCTAGG AAGAAgCTTC AGAAAnCctGA	60
GAArACaTGA TATTTsTwTy TGTAACATG ACATTGGATG CATTTGnCyG AAYAGGAaGA	120
TtGTGCTTTT CTCCmAAACC wCTTTCACGG TGATTTTTGG TTAArTtTCA CCcGAawTCC	180
ACAAsAATTT GTCCAGATAC TctGGATGAA AACAAAACTA TCTGGTGTGT TGTGGCTATC	240
TCAATCCCAG ATCTTGCTAC AGCCTCTGTG TkTGTtTGtG TTTTCTGGAC ATTCTCTATG	300
GACTTTAmGG TTTTGAATGC ATTTTAGCAk GtAmsnTTTT TGTttTCAGC TGGCAAACGC	360
TAATTGGTTC CACCTGGAGT CwAATmCkCC ACACATTCGA GTTTTCTAGG AAGAAAGCTT	420
CAGAAACCTG AGAAAACATG ATATTTCTTT CTGTAAACAT GACATTGGAT GCATTTGCCG	480
AACAGGAAGA TTGTGCTTTT CTCCAAAACC wCTTtCACGG TkATTTTTGG TTAAATTcAC	540
ycGAawwCyA CAACAATTGg TCCAGATACT CCTGGATGAA AACAAAACTA tCTGGTGwkT	600
TGTTrGCTATC TCAATCCCAG ATCTtGCTAC AGCCTCtGTG TGTGTTTGtG TTTTCTGGAT	660
ATT	663

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

AAAAAATAAC TGCGTGTCAA AACCCACACC CTCAAACGG ACCCGGCGAG CAGCGCCACG	60
CACTGCACTA CCCGCCTGTC TTA CTGAACA AAGAACGCCC TTATGCGCGC GCACCCTCGG	120
ACCTTCTGAA CGTCCCTACC ACTGAGGCCC CTTCATTCA AAATCATCCC ACTCTGCAAC	180
TAATGGCTCG CTCCAGAACC TTCCGGAAAC CCCAGTTTGC TCATCAATAT GTAGCGAGTA	240
CTCATCATGC GAGGGTGCA GCGATCTCGAA ACGTACCTTG TACGTACCAA GCCCCTCTTC	300
AAACTTCACT TCGCCCCATA ATGCGGACCG TCCCCTGCGT TCAGGGGGGA AACATCAACT	360
TTGCAACTTC TCAGAGCCAT GTTTTGGGGG GAAGCAAAAA ATTCTGGGAT	409

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

GTTCTGGCAAA TGCATGCAAT GTCATGTTTA CAAATACAAA TATCATGTTT TCTCAGGTTT	60
CTAGAGCCTT CTTCTAGAA AACTCGAATG TGTGGAGGCT TTGACTCCAG GTGGAACCAA	120
TTAGCGTTTG GCAGCTAAAA ACAAACCTT ACATGTTAAA ATGCATTGTA AACCTTAAAG	180
TCCATAGAGA ATTTTGCAGA AAACACAAAC ACACAAAGAG ACTGTAGCAA GATCTGGGAT	240
TGAGATAGCT GAAATCACC AGATAGTTCT GTTTTCATCC AGGAGTATCT GGACAAATTG	300
TTGTGGATT TGGTTGAAAT TTAACCAAAA ATAACCGTGA CAGTGGTTTT GGAGAAAAGC	360
ACAATCTTTC AGTTCGGCAA ATGAATCCAA TGCCATGTTT ACAGAAAGAA ATATCATGTT	420
TTCTCAGnTT CGGAGCTTCT TCCTAGAAAA CTCGAATGTG TGGAGGATTG ACTCCAGGTG	480
GAACCAAAGA GCGTTTGCCA GCTTAAACA AAAAGGGTCC T	521

(2) INFORMATION FOR SEQ ID NO: 594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

1063

TGCTGGGTGT TCTCTGTTTG TGTC TGCCGC TTCCTACGAC GACAATGAAT TTTCTCGCAA 60
 GAGTCGTGCG TACTCGGAGC TTGCAGAGAA GACCTACGAT GCGGGGAGAG TATGACGTCT 120
 CTGCAGAGTA CGCCCGGCTC GCTGAGGGTT TTGCGCAAAA ATCCTCGGTC TACATCAAGG 180
 GAAACTATGG GCGCGCACCA ATGCCGAGGG ACGCTATGAA CGCTGCGGGC ACCCGCCCAA 240
 GCGTGCGGCG AAAAATTGAA GCGCATCGAn TGGCGTATC CGACCGAGTA ATTGCTCGCT 300
 AnGCGAnGGC TATCAAGACC GGAGGGCTTC GCTTTTTGAC AnCCAAGCAG TACGACGTAG 360
 CGCTTCACGT GGGGCGCGTh AAGGCGTThG ACGCACTCCA AAAACGTAAA AnCTGAAAAT 420
 TCATTGCTTG CCAAAGGCCG CGAAGGAAGA AGCTGCGCGC CAAGnCGCCG AAGCACGAAA 480
 ACTCCGA 487

(2) INFORMATION FOR SEQ ID NO: 595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

ATChGTGTGC GTGCCGAGGA TGCACCAGGT GGTATGTCC CCGnGAACCC TGCCTCTCAA 60
 GCACAGGATG CAGCGTTTGA TTTGATGGG GTGCACGTTA CGCGCGGAAC TAATTCTATC 120
 ACCGACCTTA TCCCCGGCGT TACGCTTTCG CTGCACGAAC GTACAGAAAA AACCGAAACG 180
 CTCTCTGTCA CCCCCGACGT GAACGCCATG AAGAACGCTA TTATAGAATT CGTTGCTAAG 240
 TACAATCGAC TCATGGCAGA AATTAACATT GTCACCAGTA ACAAGTCAGA CCATTAThGA 300
 CGAGCTTGCG TGATCTTACC CCCGAGGAGA AAAAGAAAGA GACAGAACAA CTCGnCAAC 360
 CTCCACGGGG GAATCCA 377

(2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

CGTGCTTTCA CCTTTTCCCC ATThAAGAG AGTGTTAATA TCCACAATAC GCTCACCATC 60

1064

GTAGAACACA ATGACCTCTG AAnAAGGGTA CCGCCGCGTT GTAACCTCTG nnAATACGCT 120
TCCACGCTTC CACATTCCCC TTATGAAACA ACTCGTTAGA AACAGGCACC GATATTAACT 180
GAGACATCCG AATCGGACCT nCAGAGGCTT GAGCAGGAGG ACGCGCGGTG AGGGGGGGGG 240
GGGAGACGA AnCCCCGATCA CAGGTAGCCC CTTAGACGC CCTGGnAGCG TCCGCACCCG 300
GTTCTTTGCC GATCGAACC TCTTGCCAGA ACCCTCAGAC TTTTTCGTAG ACACAAATGC 360
nAAAAC 366

(2) INFORMATION FOR SEQ ID NO: 597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

ATTTAAAAGG ATCTAGGTGA AGATCCTTTT TGATAATCTC ATGACCAAAA TCCCTTAACG 60
TGAGTTTTCG TTCCACTGAG CGTCAGACCC CGTAGAAAAG ATCAAAGGAT CTTCTTGAGA 120
TCCTTTTTTT CTGCGCGTAA TCTGCTGCTT GCAAACAAAA AAACaCgCTA CCAGCGGTGG 180
TTTGTTTGCC GGATCAAGAG CTACCAACTC TTTTCCGAA GGTAACCTGGC TTCAGCAGAG 240
CGCAGATACC AAATACTGTT CTTCTAGTGT AGCCGTAGTT AGGCCACCAC TTCAAGAACT 300
CTGTAGCACC GCCTACATAC CTCGCTCTGC TAATCCTGTT ACCAGTGGCT GCTGCCAGTG 360
GCGATAAGTC GTGCTTACC GGGTTGGA CTAGACGATA GTTACCGGAT AAGGCGCAGC 420
GGTCGGGCTG AACGGGGGGT TCGTGACAC AGCCAGCTT GGAGCGAACG ACCTACACCG 480
AACTGAGATA CCTACAGCGT GAGCTATGAG AAAGCGCCAC GCTTCCCGAA GGGAGAAAGG 540
CGGACAGGTA TCCGGTAAGC GGCAGGGTCG GAACAGGAGA GCGCAGGAGG GAGCTTCCAG 600
GGGGAAACGC CTGATATCTT TATAGTCCTG TCGGGTTTCG CCACCTCTGA CTTGAGCGTC 660
GATTTTGTG ATGCTCGTCA GGGGGCGGA GCCTATGGAA AAACGCCAGC AACGCGGCT 720
TTTACGGTT CCTGGCCTTT TGCTGGCCTT TTGCTCACAT GTTCTTTCCT GCGTTATCCC 780
CTGATTCTGT GGATAACCGT ATTACCGCCT TTGAGTGAGC TGATACCGCT CGCCGCAGCC 840
GAACGACCGA GCGCAGsGgT CAGTGAGCGA GGAAGCGGAA GAGCGCCCAA TACGCAAACC 900
GCCTCTCCCC GCGCGTTGGC CGATTCATTA ATGCAGCTGG CACGACAGTT TCC 953

(2) INFORMATION FOR SEQ ID NO: 598:

1065

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

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CCGAAGTAAC TGGCTTCAGC AGAGCGCAGA TACCAAATAC TGTTCTTCTA GTGTAGCCGT      60
AGTTAGGCCA CCACTTCAAG AnCTCTGTAG CACCGCCTAC ATACCTCGCT CTGCTAATCC      120
TGTTACAGA GATACCTTG CGTTTTTGCC AGGCGCAGTG CGGCAATGGT GTCAGCCGTT      180
TCTCCCGACT GAGnAAATCG TCAGTACTAT TTCACGCGCG TGCACGACGC TCGTGCGATA      240
nCGGATACTC TGAGGCAATC TCCACCTGAC ATCCCACCCC TGCAAATGCC TCAAACCACT      300
AACGCGCCAC TAACCCTGAC ATGGTACGAn GTACCACACG CGATAATGCG CACCCGTGTT      360
ATCCGTCTAA ACAGCCGCTA CAAACGTCTT ACACGAGGTA nCGTCCAAGA CnCGGTCnTC      420
CCCGAACGTC CGCACCTGTG CGCGAGAAGA CGAAGAAAGA CGACATAT      468

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(2) INFORMATION FOR SEQ ID NO: 599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

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GGAAGAGGCA CACCTGACAT GGAAGGAAGC TGCGCGTGCG GCAGTAGACG CAGGAGCACA      60
AGCGCTTGCG TTGCACCCGC GCACCTGCnC CAGTGTTACG CGGGAGAGGC AAACCTGGGAC      120
ATAATCGCAG ACCTCGTGCA GTGCGCGCGT GGGTGGGGAG AGGTTCCTCGT GTTCGGCTCA      180
GGGGATCTGC ATGCGCCTGA AGACGCACGG GCAATGTTAG AACACACCGC ATGCGCGGGG      240
GTTATGTTTG CCCGCGGTGC TATGGGCAA CCGTTTATTT TCAGACAAAC CCGTCAAGCT      300
TTTAAACTGA AAGGATACTA ACACGCCCCG TGAACGTTTT GAAGCAAAAA GCTTAAGCGC      360
CAACTTGGCC GCGAAGCTTT CAACTTCTTG GCAACAAAGA ACGTTGGGGA AGAAAAAGCT      420
TCAAGCCCTT GGCAAAACCA AGAATnTCCG CCAAACGGT TTTTTTGgNT TTTCCGG      477

```

(2) INFORMATION FOR SEQ ID NO: 600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs

1066

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

CTCCAGAAAC CTGAGAAAAC ATGATATTTT TTTCTGTGAA CATGACCTTG AATTCATTG	60
CTGAACACAA AGATTGTGCT TTTCTCCAAA ACCACTTTCA CGGTGATTTT TTGGTTAAAT	120
TTCATTTCAA AACTACAACA ATTTGTCCAG AGACTCCTGG ATGAAAACAA AACTATGTGG	180
TGATTTGTAG CTATCTCAAT CCCAGATCTT GCTACAGCCT CTGTGTGTGT TTGTGTTTTT	240
TGGATATTCT CTATGGACTT TAAGGTTTTG AATGCATTTT AGCAGGACCC TTTTGTTTTT	300
CTGCTGGCAA ACGCTAATTG GTTCCACCTG GAGTCAAATC CTCCACACAT TCGAGTTTTT	360
TAGGAAGAAA GCTCAGAAAC CTGAGAAAAC ATGATATTTG TATTTGTAAA AATGACATGG	420
ATCATTGCTG AACAGAAAGA TGTGCTTTTC TCCAAAACCA CTTTCACGGT GATTTTGTAT	480
AAAATTTTAC CGGATATCCA CAAAATTTG TCCAGATACC CCTGGATGAA CAC	533

(2) INFORMATION FOR SEQ ID NO: 601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

AAAACCACTT CCACGGTGAT TTTTGGTTAA ATTTACCCCG AAATCCACAA CATTTTGTCC	60
AGATACTCTG GATGAAAGCA AACTATCTG TTGTTTTGTG GCTATCTCAA TCCCACATCT	120
TTCTACAGCC TCTGTGTTTG TGTCTTCTGG ATATTCTCTA TGGACTTTAC GGTTTTGAAT	180
GCATTTTAGC AGGACCCTTT TTGTTTTCAG CTGGCAAACG CTAATTGGTT CCACCTGGAG	240
TCTAATACGC CACACATTCG AGTTTCTAG GAAGAAAGCT TCAGAAACCT GAGAAAACAT	300
GATATTCCTT TCTGTAAACA TGACATTGGC TGTATTTCCC ATACAGGAAG CATGAGTTTT	360
TCTCCAAAAC CACTTTCACG GTGGATTTTG GTAAAGTTTC ACCCACAATA CACAACAATT	420
TGTCCTGGAT	430

(2) INFORMATION FOR SEQ ID NO: 602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs

1067

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

GAnTTGAGCA TGTCAAGTTC TnCCCTGAA GACGAGGGAG GGGATGGTTC TACCCTCAGC	60
AGGAGACGAC GGATTTTGTt GGCAGTGTGC GCATTTCTCA TTCTGCTCGG TGGTGTCTTG	120
GTAGGTTGGG TTCTGTACAT GCACGGCGCC TCTCGTCCTG CGGTCGTGCC GTCACAAAAA	180
GTTGAAGTGG CCCAGGTCtT CTGGCGGCAT GTTGCAGCGC GTGAGCTTGG AGCGTACTGC	240
GGTTGAGGCA CGTGTTTCGTC GATCTCCCAT CTGAGACTGG CTCTTCCAGA AACCCACAAG	300
GGAAAAGGGA CGTTCCCCC TGGCGTTCTT CCCGGGGGCT GAAACGGGCT AACGAGTGCA	360
G	361

(2) INFORMATION FOR SEQ ID NO: 603:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

AGCGnGnAGA GGATCCCGTG TACAGTGTA ATGGCTGGTG GTGGGATTTA CGTAAACGTC	60
GTATGCGCCT GTCACGTGGC GCACTGCTTC CTCTATGCGC CGCACGCACG CAGnAAGCAT	120
ATACCGTGAA CAACAAATGA CACTTGCATG AAAGACTACC TCCTATTTCAG GACGGGTTTT	180
TTATGTATCC AAAAGCTCTG GGGAGGnAAC GGCTGGCAGT GACGGCAAGA AACTTGCATG	240
TACCGGTTAA AAAACCGTAC ACTTTTCATC CTATCTnGCT GTGAAATGGG AGCTCAACGA	300
ATTATGACCC AAAAACTGn CAAAAAATAG TGCTGCCT	338

(2) INFORMATION FOR SEQ ID NO: 604:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 959 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

1068

CGGATnCCGA CTGCGTAATT TTGAATCGAG GAGTACAGTG ATGGAGACGT TTTTACCTC	60
AGAGTCTGTG AGTGAGGGTC ATCCTGATAA GCTGTGCGAC CAGATTTC TG ACGCTGTTCT	120
TGATGCCTGT CTTTCGCAAG ATCCTCACAG TTGTGTTGCG TCGGAAACTT TTGCCTCCAC	180
GTCCCTTATC CTGATTGGAG GTGAAATTAG CACGCGGGCG CATATTAATC TTACCCAAAT	240
TGCGCGTGAT GTTGCCGCTG ACATTGGATA TGTAAGCGCT GATGTCGGTC TTGATGCAGC	300
GTCCATGGCT GTTCTTGATA TGACTCATCA TCAGTCGCCT GATATTGCGC AGGGGGTGCA	360
CGGTGCAGGA CTGAAGGAGT TTGCAGGATC GCAGGGGGCA GGGGATCAGG GGATTATGTT	420
TGGTTTTGCG TGCCGCGAGA CGCCGGAGTT TATGCCCGCC CCCCTCATGT GCGCGCACGC	480
GGTTGTGCGC TATGCTGCCA CGCTTCGTCA TGAACGCCGT GTGCCGTGGC TCGTCTCTGA	540
TGCAAAAAGT CAGGTTACCG TACAATACGA GGGACATCGA CCGGTACGTA TCAGTGGGT	600
TGTGTTTTCT CAGCAGCATG ATCCGTCACC TTCATACGAA ACCATTAGAG AAACGCTCAT	660
AGAGGAGATA GTGCGTCCGG CGCTTGCACC TACAnGTCTG TTAGATGAAA ACACGCGTTT	720
TTTTATCAAT CCAACCGGTC GTTTTGT CAT GCGGGTCCCT TnGGGACAnT GGTTTnACCG	780
GGAGAAAGAT CATCGTAGAC ACGTATnGGG GAATnGGGCG CCATGGAnGA GGTCTTTTCA	840
GTAAGGTGC ATCTAAGGnA GATCGTCTGC AGCGTATATG CGCGTATATT GCAAAAAAAT	900
TTGGCAGCCG ACCTTCTGAC GcGTTAGTG CAGCTTGCAT ACGCAATCGG GGTACAnAT	959

(2) INFORMATION FOR SEQ ID NO: 605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

AGTATGCCCC CGCGGCAAAT GAAGACGnAA CGTGACGAAA CCCTCGTGCT ACTCAGTAAA	60
ACCCGAGACC CTGACCCGAC AGACCGnCAG CCGCAGACCG GCAGTGCAAC AACGACATCT	120
TATAGGATGG CAGGCGTACA TGCCCGTCCA CTACACGGTC CTGACCGGAC CCCAAGCCCC	180
AGCCGCAGCC AACATCAACT TCCCGGTATG GGGATGCCTC ACGCACATCG CAGCCAGCAA	240
TGTATTTT CAG GGAGTATTTT TCAACATGGC CATGACCGGC ACACGACTGC GCCAGCCTCG	300
TGGGGCGTAA GAAAGACGGA GCGCAGGCAC CTnAGTCGAG GACTGCGTGA ATGTGGAAnG	360
CTCGTTTAGC TTCTCAGA	378

1069

(2) INFORMATION FOR SEQ ID NO: 606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

```
CCACCCnTAT CAGTTACATC AATGGGAAAA CCATCGCACG CAGCAGCACG CAACAAGAAC      60
ACTTCCGAAT GCTCCCGGCA CATATCGTGC GCAATACCCG CGCAATAAAC GTGCGGCTCA      120
AGCTGCGCTT CCAACGCATA CCGCCGTACC AGCATGCACC CAAACTCCGC TACACGACGC      180
GAATGCTCAT GCTGCACCGT CTCGGCAGTA TACGAAATAC CCCCACGCCT AATCTCACAC      240
TCTTCAACAG AAAAATACGG CGTTGTCCCA ATTGCTAAAT GGAGCATCCG CACCCGATCG      300
TGCGCACTTG CACTTCCTTC CTTTCTTTG AAGGGGAAA CGAnGTAGGC ACAAACAGCA      360
CGCGGTCATA CCCGGCGTGC GGTGTACTGG CATCAGCCAA GAGCAAGTGG CCCAGATGAA      420
CAGGATnGTA CGAACCGCCA AACAG      445
```

(2) INFORMATION FOR SEQ ID NO: 607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

```
GCCATTGCGC ATTCAGGCTG CGCAACTGTT GGGGAAGGGCG ATCGGTGCGG nnCTCTTCGC      60
TATTACGCCA GCTGGCGAAA GGGGGATGTG CTGCAAGGCG ATTAAGTTGG GTAACGCCAG      120
GGTTTTCCCA GTCACGACGT TGTA AACGA CGGCCAGTGC CAAGCTTGCA TGCTGCAGG      180
TCGACTCTAG AGGATCCCCA GTCTTTTCAG ACTGTCCGCA TCATTGGGCA AAACGATGAG      240
CGCAAAGTAC TTACCCGAGA CACTCGCCCCA AGAGACAGGC GTATCTACCT GTTCACGTCC      300
ATCTCCTTCA GAGCATACGT TTTCGCCTGC CAACTGCACT ACCATGAAGT GCGAAACTCA      360
TATTGTCCGC CGCATCCGCT CAGGCCCGAT CTCAGGCGGT GTGCGCAGGT ATAAnTGCTG      420
TCCAAGTCA AAGCC      435
```

(2) INFORMATION FOR SEQ ID NO: 608:

1070

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

```
CTnCGGCAAC GCATACAAAA CACCGTCGnC GAGTTTTTTC AACTGCGCGT CATTCTCCAC      60
AATTACGGTG CGTGCCTCTA CCGCACCGAG AATCTGACAC AAGATCACGC TCGGTAGCGT      120
CAGAGCCACG CGGTGTACGC TGCTGCACCA AGCGCCTGAA TACCAAAGCT CGCGTGGAGC      180
CACTCAACCC GATTGTCCGA AATCAAACCA ATGTCAATCA CCACGTACCA CACCCAATGA      240
CTGGCCAG                                         248
```

(2) INFORMATION FOR SEQ ID NO: 609:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

```
CAGAGGCTGT AGCAAGATTC TGGGGATTGA GATAGCTACA AATCACCAGA TAGTTTTGTT      60
TTCATCCAGG AGTTTCTGGA CAAATTGTTG TGGATTTCCTG GTGAAGTTTA ACCAAAAATC      120
ACCGTGGAAG GTGGTTTTGn GAGAAAAGCA CAATCTTCCT GTTTAGCAAA TTCATTCAAT      180
GTCATGTTCA CAAAAAGAAA TATCATGTTT TCTCAGGATT CTAAAGCTTT CTCCTTAGA      240
ACACTCGAAT GTGTGGGAGT ATTTGACTGC AGTGGGACCA TTAGCGTTTG CCAGCAGAAA      300
ACCAAAAAGG GTCCTGCTAA AATGCATTCA AAACCTTTAA AGCCATAGnG ATATCCn      357
```

(2) INFORMATION FOR SEQ ID NO: 610:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

```
GTGAGTTTTC GTTCCACTGA GCGTCAGACC CCGTAGAAAA GATCAAAGGA TCTTCTTGAG      60
```

1071

ATCCTTTTTT TCTGCGCGTA ATCTGCTGCT TGCAAACAAA AAAACCACCG CTACCAGCnn 120
 GTTTGTTTGC CnnAATCAAG AGCTACCAAC TCTTTTTCCG nAGnAACTGG CCTTCAGCAG 180
 AGCGCAGGGG ACCAAATACT GTTCTTCTAG TGTAGCCGTA GTTAAGGCTC CCCACGnAAC 240
 ACCGTGGTGC AGGCGTCAAG CGAATTGAAT ACCATGTTCT CTATCGCTGT TTCTGTGTAG 300
 AAGGCGATAT GAGGGGTATA GATGATACGC TCATGTnCGA CAAnCCGAGC ATAGACCGTA 360
 TCGTAATAGG 370

(2) INFORMATION FOR SEQ ID NO: 611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

TGGTTAACCC CCCACCATTG GCCTTAACCC CCCAAGGCC CGGTTTGGAA AAAAGGGACC 60
 CACCCTTAAT TCCCCAAGG CCCAAGAGGG GGGGTTTAAC CGGGGGTTCC CAAGGGGGTT 120
 CCCAAAAAA GGAAGGGAA TTGGGGGGAA AAAAAAAGG CCCAACCCAA GGGAAAGnGG 180
 GCCCGGAAT TTGGGGGGAA ATTCCCCCTT TGnTTTGGG CCCTTTTnA ATTTCCCAA 240
 GGCCCAACCC GGGCCCCCA AAAACCTTT AAAAAAAGG AAGGTTTCCC CCCAAAAACC 300
 CGGGAAATTT GGGAAACCG GCCCAAACCG GGTnTAACC GGGGAACCCn AACCTTTT 360
 GGGGAACCT TTTTCCCTT CCCGGGTTG GnCCGGGTTT AAGGATTGG GAAAAA 420
 AAAAGGGAA AAAGCCCGG GCCGGGCCC CGGGTTTAA CCCAATTGG nCCAAATTGG 480
 GGGGCCAAG GnCCGGGCC GGGGGTTnA AAAAAAAGG ATTTCCCCCA AGGACCGGGT 540
 T 541

(2) INFORMATION FOR SEQ ID NO: 612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

CAATTTTGTG GCGGTTATGG CTACGGnTGA nAGTACTTGC AGGAACCGGC CCACAGTTCA 60

1072

GGAGGGCCTC GAAGGCGAGG CCCGCGGTGA GTGCGCCGTC TCCTACGACA GCGACTACCT 120
TACCTGATTT ACCCCGGTAT CGTAGGGCGC TGAGGATACC ACTTGTCGGG CAGAAAGTGC 180
CGTGGAAGAG TGACCGGTAC CAAAAGCGTT CGTACGGGnC TTnCATACG TCGCCGCGGG 240
GAACCCCGnA AATCACCATC CTTCTGGACG GTAGGGTCAT GGGAAGCGGC CCTGGCGCGT 300
GCCAGTGAGG nAGCTTGTGC GACGTACACT 330

(2) INFORMATION FOR SEQ ID NO: 613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

TGGCTGTTC ACTTCTGATC CAGCTCCCTG CGACTGGCCT GGGAAAGCAG AAGATGGCCC 60
AAGCGCTTGA GCTCCTGCAC CCACATGAAA GACCCAGAAG CTCCTGGCTT CTGATCAGCC 120
CAACTCTGGC TGTTGCAGCC ATTTGGGGAG TGAACCAGTA GATGGAAGAA GATCTAACTC 180
TCCCTCTCTA ACTCTACCTT TCAAATAAAC AAATATTTTC TAAAAATTTA TACTTTTGCA 240
AAAAATCTGG TCAGTTTATG TGGTTCCAGA GTAATTATAA TATTGTTAGA ATTACTCTTT 300
ATTCTTAGTG TTTATTCTGC TGTATTGAAA TCACTTGGAC AGGATCTGGG AAGAAACCAG 360
CCAAGGAAAG AGGAAACAGA AGTAACTCT TAAATTCTGT AATTCTTAAT AGATTATTTA 420
TTTGAGAGGC AGAGTTAGAG GAGAGACAGA AAGGTCTTCC ATCTTCTGGT TCACTCCCTA 480
AATGGGCCAC AATGGGGCAG AATTGGGGCC AATGGCCAGG GAACATCTTC CAGGTCTCCC 540
TTGTGGGTAC AGGGGCCCAA GCACT 565

(2) INFORMATION FOR SEQ ID NO: 614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

TGTGCCTTTT ATCTCTTCTT GGGCCCTACT ACTCAACAAC ACTGATTTTA AAAAATTATA 60
TTGAAACAAT ATCAATATTA GCGTTTTTCT AGGTTTTTTA CATGTGTTAT CTCACCAATA 120

1073

TTTACAAAGA AGATCCTAAA CAATACAGAT AACACCAAGA CCAAAAAAAAA AAAAAAGTAA 180
TATATGCCAT TAGTTTAGAA ATTCAAACAA TATAAAAGAC ATAAAAAGCA AAAACAGAAG 240
CAACTTGGTT TCCATCCCCA AAGGAAACAG CACCAACAAT TTTTTTTTTT TTTTTTTTTT 300
TTTTTTTTTTA CAGGCAAAGT GGACAGTGAG AGAGAGAGAG AGAAAGGTCT TCCTTTTGCC 360
GTTGGTTCAC CCTCCAATGG CCGCCGCGGC CAGCATGCTT GCAGCCAGTG CACCGCGCTG 420
ATCCAAAGCC AGGAGCCAGG CTGGCAACAG ATGGCTGGCA ACAGATG 467

(2) INFORMATION FOR SEQ ID NO: 615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

TGCGATGCCT GCAGGTCGAC TCTAGAGGAT CCCCGGGTTC GTACGTTTCGT CTTATTTCCG 60
CGCGGGCATA CTCAGCAATA TTCTGCCTTC CACTTCGTAG GAGCAGCAGG AGCAGCAGGG 120
GGCGTGGCCT TTTGTTCGT ACCGCCGTAC 150

(2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

TGCCTGGGTT CAAGTCCTGC CTCCTCTACT TGAGTTTCCG CTCATGTGCA CCCCAGGAGG 60
CAGCAGATGA TGCTGGCTCA AGTACTGGAT CCCTGTCCCC CATGTGGGAG ACCCAGACTG 120
AGCTCTGGGC TCCTGGCTCC AGCCCTGGAT GATACAAGCA TTTGAGGAGT GAACCAGAAG 180
ATGGAAGATC GATCTCTCTC TCTCTCTCTC TTTCTCTCGT GTGCACACGC GCACGCATGC 240
TCATGGCCTG TCAAATAAAG TGAAAAAAGA AATCTGTGCA CCCAAGATTT ATGCATCTAT 300
ATATGTAAAC TTTCTTTCAA TTAAGAAACA TTAGGGGTCA GCATTGTAGC ACAGTGGGTA 360
AAGCTGCCAA TCGTGACACC GGCATCCCAT GTGGGCGCCG GTTCATGCCC TGGCTGnCTC 420
CACTTCTCAT CCAGCTCCCT GCTAATGGCC TGGGAAAGCA ACAGGTGATA ACCCAAGTGT 480

1074

TTGCGTCCCT GCCACTCAGG TGGGAGACCC AGATGAAGCT CTTGGTTTTG GCCTGGCCTA	540
GCCCTGGCCA TTGAGGGCCA ACAGGGCAGT GAACTACCAG TTGAAAGGTA TCATGTGCAC	600
TGGGCTCTCA CGC	613

(2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

GTGGGTGCAG GGGCTCAAGG ACTTGAGGCA TCTTCCACTG CTTTCCCAGG CCATAGCAGA	60
GAGCTGGATT GGAAGAGGAG CAGCCAGGAC TAGAACCGGC ACCCATATGG GATGCCGGCG	120
TTTCAGGCCA GGGTTTTAAT CCTCTGCACC ACAGTGCCAG TCCCAGTGTT GCAATTTTGA	180
TTGGTGTnGA CTTTCTCAG	196

(2) INFORMATION FOR SEQ ID NO: 618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

GTATTTGAAA GGCAGAGTGA CAGGnGGGAG AGAAGGAGAG AAAGAGAGAA AGAGAGAGAG	60
AGAGAAAGAG AAAGAGAGAG AGAGAGACTG CCCATTCTCTT GGTTCACCTC CCAAGTGGCC	120
ACAAGAGGCA AGAGCCGGGA CTGGGCCAGG CAGAAGCCCG GAGACAGGAA CTCCATACAG	180
GTCTCCCATG TGGGTGACAG GGGCCCGAGT ACTTAGACCA TCATCTGCTG CTTTCCCAGA	240
CACATTAGCA GGGGACTGGA AAGGAAGCAG AATAGCCAGG AATCAAACCA GTACTCATAT	300
GGGATGTTAT TATCATAGGC AGTGGCTTAA CCCACTGTGG CCACTATGTC AGCCCCATAA	360
CTGGGCTTTT TTATTAAAGC AGACACATTT TGGCTGCCC TGTCTACCTC TTAATCTACA	420
TTTTTTCATC ACAGCATAAA GAATTGTCTT TATTCATGTA CTCTCCCAAG CCTAACTAAA	480
TAATCATATA TTAAATAAT TCATCAATAT AGACAAGCAA GAAATTTTAT CTTTCTAGAGAA	540
TTTATGTGTT AGCATAAAAG AGAAGAGAAT GGGGCAAAAT GTGTCCAAAA ATCTTATCCT	600

1075

TTT

603

(2) INFORMATION FOR SEQ ID NO: 619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

AGAGCGGTCT	TCCAACCATT	GGTTCCTCC	CCAGTTGGCC	GCACCGGCCA	GnAGCTGTGC	60
CAGTCCGAAG	CCAGGAGCCA	GGAGCCTCCT	CTGGGTCTCC	CATGCAGCTG	CAGAGGCCCA	120
AGGACTTGGG	CAATCTTCTT	CTGTTTACCC	AGGCCATAGC	TGAGAGCTGG	ATCGGAAGTG	180
GAGCAGCCAA	GACCCGAACC	AGTACCCATA	AGGGATGCCT	GCACTGCAGA	TGGCAGCTTT	240
ACCTGCTACA	CTACAACGCC	GGCCCCATCT	TTCTTTATTA	TTGAAGTATA	GGAGCTTTTA	300
TATGGTATGG	AGACCAGTTC	CTTGTCAGAT	ACATGGTTTG	TAAATATCTC	CTGTTCTGTA	360
GGTTTTTTGC	TTTCTTGAT	TTTTTGAAAT	ATAAAAGTTT	TTTAATTTTG	ACATCTGATT	420
TACCTACTTT	GTGGTGATGG	TTATACTTTT	GATATTATAC	CTAACAAACC	AAGTCACAAT	480
CCAAAGTTAC	ACAGATTTAT	ACCTGGTTTT	CCAAGAATTT	TACTGTTTTA	GCTTTTTTTA	540
TTTTAAAGGn	TTATTTATTT	ACTTGAGATG	CAAAGTTATA	G		581

(2) INFORMATION FOR SEQ ID NO: 620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

CTTGAAGGGG	TGTGTTTTCT	CAGATCATTT	GGAAAATTC	TTCCATAGAT	GCGTGGTATT	60
ACTAGCACTC	TGTGTGCAAG	TCATTCTCTC	TTTTTTTTTA	AAAAAAGAT	TTATTTATTT	120
ATTTGAAAGG	CAGAGCAACA	GAGGGAACAA	GAGACAGAGT	GAAAGACAGA	GAAAGAGATC	180
TTCTTTCCAC	TGGTTCACCT	CCCAAATGGC	TACAACAGCA	GGGCATTGGT	CTAAGCCGAA	240
GCCAGGAGCC	TGGAATCCA	TCCAGGTCTC	CCACGTGGGT	GGCAGGAGCT	TCCACTGCTT	300
TCCCAGGCTC	ATTATGAGGG	AACTAGATGT	GAAAAGAGCA	GCTGGGTCTT	GAACTGGTGC	360

1076

CCTGATATGG TTTGCCAGCA TCACAAAGTT CTGACTTAAC AACTGAGCC ACCATACCAG	420
CCCCCAATC ATTTCTTTTC CCTATTGTGC CTATCTGTCA TACATTCCTT TTGCTTATCA	480
TGCATTGTG TGCTTTGCAA CAACTGATT AATTCAGGAA CTGTCTTTAA CTCACTGGC	540
TTGTGATTAG ATTAAAGGT AAAGGGACCT GCCCCTCCTA GAT	583

(2) INFORMATION FOR SEQ ID NO: 621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

TGTCCTCCT TAAATATATA ATAGTAATTA TTATTTAAAG ATTTATTTAC TTATTGAAA	60
GGTAGAGTTA CAGAGAGAGA GAGGGTGAAA CACAGAGAAA GAGAGGTCTT CCATCCACTG	120
GCTCACTCCC CCAATGGCCA CAATGGCTTA AGCTGGACTG GTCAAAAGCC AGGAGCCAGG	180
AGCCAGGAAC CAGGATCTTC CTGCGGTCT CCCATGTGGG TGCAGGAGAC CAAGCACCTG	240
GACCATATTC CACTGTCTCC CAGGCACATC AGCAGGGAGC TGGATTGGAA GAGGAGCAGC	300
CAGGACTCAA ACCAGTGCCC ATGTGGGATG CCGGCACCAC AGGTAGAGGC TTAACCTAAT	360
ACACCACAGT GAGAGCCCCT AATTATTATT TTTATATTTA AAATAAACT TAAAAGAAAA	420
GACATACAGA TAGGAAATAA GCATTGAAAA ATATACTCAA CATCATTAGC TATTAGGAAA	480
ATGCAAATTG AATATCCCAAT GAATATGACT GAACATCTAC TTACAATGGA CATATTTAAA	540
ACCGCCCTTT GTGACATTCT GTGTATTTTT CAGAAACCAT AGAATTGTAT A	591

(2) INFORMATION FOR SEQ ID NO: 622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

GAATAAAATA ATGAAAGCAT ATCTTCTTTA GTCATGTTTT TTCTTGTTGA ATTATATTGA	60
GGGGTTTTAA TTGTTACCT AAATAAGCA ATGTTTTATT GTTTTGAGTG TTATTTTAAT	120
GTTTCTGTGA AATTTTCTA ATTTATATCA CACTTTTTTT TAAAGATTTA TTTATTTTGT	180

1077

TGT TTGAAAG GCAGAGTTAC AGCGAGAAAG AGGGAGATAC AGAGAGCTCT TCCATCTACT 240
 ACTTCACTCC CCAAATGGCC AGAGCTGGGC CATTCCACAT CCAGGAGCTA GCAGCTTCCT 300
 CTGGGTCTCC CACATGGGTG TAGGGGCCCA AGTACTTGGG CCATCTTACA CTGCTTTCCC 360
 AAAAGCATT A CCTGGGAACC CGATTGGAAA TGGAGCTACC GGGACTCAA CTGGTGCCAA 420
 TATGGAATGC CAGCACCACA TGCAATGGTT TTGCCCCCTA TATCACAGTT TTGTGTCTTT 480
 CTGGCTTCCC TCTCTCCCTT TATCCTGTTT TTCTTTTAA AATTTT TTA GTTTTTGnC 540
 TTTTAGACAG TGnTTTGTAC TTTG 564

(2) INFORMATION FOR SEQ ID NO: 623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

AATTGATTAA TTAAAAAAT TATGTCTTCC TGGAGAATTG TTCCATTGT TATTTGAAAT 60
 CTGCCCTGTC TGAAATTAAC CTAGCTACTC TTGCTTTATT TATTTATTG AAAGTCAGAA 120
 TTAGAGAGAG AGAGATCTTC CTTCCACTGG ATGACTCCCA GATAGCTACA ACAGCCAGGA 180
 CTAGGCCAGG CTGACATCAG GTGCTGGGAG TTTTCATCCAG ATCTCCCATG TGAGTTGCAG 240
 GTATCCAAAC ACTTGGGTCA TCTTCTACTG CTTTCCCAGA CCATTAGCAG GGAGCTGGAT 300
 TGAAAGTGA GCAGCTGGGA CACAAACCAG TGCCCATATG GGATGCTGGC ATTACAGACA 360
 GCTATTTTAC ACCCTATGCC TCAATGCTGG GCCCAACTn CTGCTTTCTT TCAATTAnGT 420
 GTTA 424

(2) INFORMATION FOR SEQ ID NO: 624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

GCCCGACTGT ATCATTCTT GAAGGTATAA TTTAAAGGC CTTTCTCTGG GAAGCTTCTG 60
 CAGGTTGCAG ACAAGTGTA TTCTGCCTTC CTTGTGCCCC ACTGCTTAGT TGAGCCCCTA 120

1078

TTTCAGCGCT CACTGCTGTA TGCTATCATT TACCTCTTTG CGTGTCTGTG TTGCTCCCAG	180
GTCTGCGAGC CTCTGCGGTG CAGGCAGGA CTGTATCTTT ATTACCTCT ACATCCATCA	240
GCAGCACCTA GCACAGGACC TGGTATTACA TGTTGAAAGA ATGTGTTTCA AGATTCAAAT	300
CAATTTTTTG TATTGCTTCT AACTTTCAAT ATAATCATG GTGCATGCTC TAAAACCTGA	360
GCCCTTTAGC TCATAGAGAA TTTATATTAA AGTTATGAAT TATATAGATG TGTATGCATA	420
AACCTTGTTT TTTAACTGGC TGGGATCATC CTTTTTTAAA GATTTATTTT ATTTATTTAA	480
AAGACAGAGT TACAGAGAGA GGTAGAGATA GAGACAGAGA GAAAGGTCTT CATCCATAGT	540
TCACTCCCCA AATGGGCTAC AGTGGGCCAG AGCCAACCCA ATCCAAAGCC AGGAGCCAGG	600
AGCTCTTCCG GGTCTCCAG TGGGTGCAGG GGTCCCAAG ACTTGGGG	648

(2) INFORMATION FOR SEQ ID NO: 625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

CAGGCTTGTA ACAGTTCTGT TTTATGCAAT GTCGGCGCAT TCAGTACTAT CGCTTTTGGA	60
CGCGCACCTG ACGCGCGCGC TATGTCTTCA CACAAAAGAC GGGTAACTTT CGGTAACAAA	120
AACTCTTCGT GCTGCTGCAG TAGTTTAGGC TCAGAGAACA GTAACACACC CAAATGCGCA	180
GAGTGCAGGC CGCCATCTTT ACGCCGTAAC GAAAGGCCGC GCGCACCGCA GCCACTTGAA	240
ACCGCTCTAC TATAGAGTCG CCATAAGATT CAAAAGTTC ACGCGTGC GCATnCCGCG	300
TTCAATACAG TAACATCCCC GTTCTGCAAG CAGGCGCGAG ACCACATTCT TCCCCGCACC	360
ACTnCGACC GATGACACCA ATTAGTGGAC AAAACTCGCG CACAGCGAGA GCGTnAACGT	420
CAAACACGCA CCGTCCTCAA GTGTTCAGAA TGTGCTGAAC ACCCGATATT CCTGCGTATC	480
TTGCGCTGAC TACCCCTGTG CCTCACGCGC AGACGnCAA AGACGCTTCT GTGGCATACT	540
GTTGCTGTCT GGCACGGTTG GGAATAAACT CACGCTTGAG ACGACACAGC CGTTGCGCTG	600
CTGTTTGCAT ATCCGCATCA AAAATCCAGG GCAACACAG CGAGCGCCGG TTTCTGTCA	660
GTTCTGCGTC ATGAATTCTT GGTAACACAA AACAACGCCC ACTGAC	706

(2) INFORMATION FOR SEQ ID NO: 626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs

1079

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

CACTGGGCGC TGAGCTCCAC CTTCTCGAAG GGACTGAACG TCATCCCACC TGGTACTGGA	60
GCGCTCGTTC ATTCAACAGG TTGCCC GCGG GGTAAATAAT GTTAAAGCGA TTGGTTGTGC	120
CGAGCACGGA TGTGTGTGGT GCAAGCCAGG CGTGGGAACC GAGGGGGATG CGATACTGCA	180
CCACGCCTTC CCCAAAATTG GCATATTGAT AGTCCCAGGG GGCACAGCTC CATTcAGTTC	240
GTACCCTcCG TTATTTcTGT AACGGATGTA GGTGAGGGGG ATGTACACGC GTGCTTCGAC	300
GCCGGCGTTC AGGCCGGTGA GCAGGTGGGT GTAGGGGTCA CCGCTTTTGG TTTCGAGCTT	360
AAGGAATCCG GCAAAATCAA AGTAGTGCGC ACGAGTGGTA GCAAAGACGC GTTTGCCAAA	420
GATATTAGTG CCTGCGGTGG CAAAGTATAT GCCAGAAGAG AGCCACTTCC ACTGcATACG	480
CAgGAGCGCG TCTATGTTGA GCGCGTTCAT AGGTGCGCGC TCAAGGAAAG CGAGAAGTTT	540
AGCAGTGACA ACTCTTGGAT CGGAAGAGCG GAAGACATCA CGTACTCCTT GCTCTATGTT	600
CGGTACAAGT TGCGATACAA GCGCCGCGAG CGGCCCAgGC TaGCACGGTT TGAATGGCGC	660
TGCCGAGCGT TCCTTCTGCA ATCAAAGCAG CAAGTCCTAC CATCTCTATG AGAGTGGTTT	720
GTTCGGTGAT TCCTGGTGGC ATCATGATAT TGGGGAAAGT TCTGCACGAG TTTTCCCTnC	780
CAACCCGTCT AAACACTTTC CCTTGnTTTG AGGATAGCTC TCTCTTGGGT CTGAnGCATG	840
TGCGTTACTC TGGTGTGGn TAnCGGCGTC GAAGGGCGAA GAAGAAACGG AACCCGGCGG	900
CCTGGTTCGA GGGTGAATCG GCCTCCTAAT CCCACAGGA ATGGCGGTTT TGGTTTTTCG	960
TnCTTGGGAn GT	972

(2) INFORMATION FOR SEQ ID NO: 627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

CCATGCCCCG AAGTACCCCC GCTTGCATCA CCTGCCTGCC CACTCACTCC CCCTCCTCTC	60
ACTTCTACCT CACCCCCCCC CACCCGTCTA GCCGCGTGTG ACTACCAGGA GAGGGTGACG	120

1080

CCGCACACGA TGC GGCCGAT TCCCTGGGTG AGGCACTCGG ACACCAGCCA GGTACGGGAC	180
ATCAGAGAGC ATACCCTGTT CCCAATCAAG GGAGAATACC GTCTTCTCTA TGAGACTGGC	240
TGAAATACCA GCACGCAGCT GTGCACAGTA CTCCTTGGTT AGATAGGTAG CTCCTACTGC	300
TCCACCTGCA GCAGGGGCAT TCAGGTGTGC ACGGTGGTA GAGGCATGGA CCGTAACGCT	360
TGGCTTCACC CAGCCGTAAT CCTGCACCGG GATGCGATAC TACACCACGC CTTCCCCACC	420
ACCGGTGGAC GGATATACTC CTTTTCCTGA ATGCCACGCA CAGCCGTCCC CCCGTTATTT	480
TTGTATAGCG CATAGGTGAG GGGGATGTAC ACGCGTGTTC CAACGCCGGC GTCCAGGCCG	540
GTGAGCAGGT GGGTGTAGGG GTCACCGCTC TTAGTTTCGA GCTTAAGGAA TCCGGCAAAG	600
TCGCCACAGC TTGCGATGGT GTTATCTAAC ACCCTGGTGC CAAAAACGTT TGCCGGTGCT	660
GTGGCAAAGT ATATGCCAGA AGACAGCCAC TTCCACTGCG CCGTAAACAG CGCATCGAAG	720
GCGACATTGT AGGTGTCAAG ATACAGACAC ACGGCGCTGA CTCCCATTAG AAAGGCACGC	780
CATGCAGACG CACGCAGGTT CTGTATAGCC TGACGTATCT GCTGCCCCGC GTCCAACGCA	840
TCCGTCTTCT TCTTCACTTC TTCGGTTACA AACGTCTGAC CCTCAGTGAA AAACCTTGTA	900
GCCTCAGCCG T	911

(2) INFORMATION FOR SEQ ID NO: 628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

GTACTCTGGT GTTGGTTACC GCGTCGAGG GCGAAGGAGA AGCGGAACCG GCGCCTGGTT	60
CGAGGGTGAG TCGGCCTCCT ACTCCCCACA GGAGTGCTGT TTTGTTTTCG TTCTTGAGT	120
CTTCGGTACC CTTAACGTAT TCTGGTCCAG TGTGGCATTG CCTGCCAGCT CCAACGTAAG	180
CAGCCGCTGA CCGTCGACGC CATAGGAAAG CGTTGCATCG GCCCGAAGC CATACTTGCT	240
GTGCGTGGTG TCAGTACTAT CCCAGGCACC ATTGGAAAGG AAGGAGAGGA AACCGATGTC	300
CACATCTACT CCGCTGTTTC CCACATTGTG GGGCCTGGTA GCCGAGTTT GACCCCGGAG	360
CCGGAGAAAC CAGGGGGCAT AGCGAGTGTC CTTTCTGGA ATAGGACACG GGTGACAAAG	420
GGTTCCACA GCTGGGGCAA AGTTAACCAC ACAGGGAAGG ACTGGTACCC ACTGTTTCAGG	480
TAGGCCCCAT AACAGTGCAG GGTGCCTGG AAGGAAGCGG TAGGTTTGGT AAAGGACAGG	540

1081

GCCGTTGAGC TTTTAGAAGA CGCAAGCTCT ACTGCCAGGT CCTTCAGCTG CAGCTGTGCC 600
CCACACCCCT GAGCGTGGCC TTCCCCTC 628

(2) INFORMATION FOR SEQ ID NO: 629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

CGGATACCCC TACTACCATG CAGCGTATTA CTGCTGATGT CACCGGTGAT GTGACCGTCT 60
CTACGGTGAA TCTACCCAGT GAAGAAATGA AAGGACGCAT CATTGGGCGC GAGGGACGTA 120
ATATCCGCGC GTTAGAGACA CTCACTGGTG CTGACGTTGT CGTAGATGAC ACACCTGAAG 180
CTGTCGTCAT TTCCTGTTTC GACCCGGTAC GCAAAGAGAT TGCGCGCATC TCTCTTGAGC 240
GTCTTGTA CT TGACGGTCGA ATCCATCCGG CGCGCATTGA GGAAATTGTG CAGAAGGTGA 300
CGCAGGAAGT TTCTCAAAAA ATCTATGAGG AAGGGGAGAA AGTGCTGTTT GACCTCGGTA 360
TTCACGATAT GTGTCCCAG GGGGTACGGG CACTGGGGCG CCTGTATTTT CGTACAAGCT 420
ACGGACAGAA TGTA CTCTAC CACTCAAAGG AGGTGGCTCT GCTCGCTTCC ATGCTCGCCT 480
CGGAAATCGG CGCAGATGTT GCCATTGCCA AAAGGGGCGC GTTGnTGCAC GATATTGGCA 540
AGGGAATGGA AACTGATTCA GACCGCAAnC ACGCAGAAAT TGGTATGGAG ATGGCTCGCA 600
AAATGAATGA GGACCCGCGA GTGGTAAACG CCGTTGGTTC TCACCACAAC GACATAGAGn 660
CGTGTGTGTG TGAGTCnTGG CTCGTTCAGG T 691

(2) INFORMATION FOR SEQ ID NO: 630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

GTCCGTGCTC TGCGGGGGAA ACTTGGTTCG CTGACCATCA TCGCGTTGCC CGTTATCGTA 60
GCTGTTGTCG CAGGGGGTGT CGGCTCCTTT TCCCTGCCCT ACGTAAAAAT GATTACGCTT 120
TTCGTGGCA GAGTTATCGC CACGTTTCAT GCGCTCCAGC CATTACTCAT GAGTATCCTG 180

1082

CTGTCCATGT CTTTCTCGCT CATCATCATC TCCCCTGTGT CTTCCGTCGC GGTAGGAATC 240
GCCGTGGGGC TCACCGGTCT GGCAAGTGGA GCAGCAAACA TCGGCGTCTC CTCCTGCGCC 300
ATGACCCTCA TTGTGGGAAC CATGCGCGTC AACAAGATCG GTGTTCGGTT GGCGATGTTT 360
GCAGGAGCGA TGAAAATGCT CATGCCAAAT TGGATCCGGT ACCCGATTCT CAATATTCCG 420
CTCCTGCTCA ATGGCCTCGT TTGCGGCGTG CTCGCGTGGC TTTTCAATCT GCAGGGTACT 480
CCTGCAAGCG CAGGCTTCGG TTTTATTGGA ATTGTTGGAN CGATCAACGC CTACAGGCTT 540
ATGGCGTAAA ACTCCTATGG TGC GCGCGGG TATTCTTTTC CTCGTGTATT TCGTTCTTTC 600
CTTTCCTTGG CTGCGTAnCT TAATGAnTTT AT 632

(2) INFORMATION FOR SEQ ID NO: 631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

CCACTCGAGC GCGAGCATGn ACGTTTTTCG TACAGGTAGC GAAGTCTTAA GGTATTTAGC 60
GCACAGAACG CTGTTTCCGC AGCAGAGAAC AACATGGAAA GCACCAGCAG CACTACCAAC 120
ACACCGAACG CAGCGGAAAC GGAAAGAACA CTCACACGTA ATTCCCCGA AGGCTAAAAC 180
ACCAGAACCG AAGAGACAAC GCCATACATC CTTGGACCCC TCCCCGCTGG GGGGGGGCAC 240
CTTTTAAGGT GCTCAGCCCC TTGTGTCAAG AGCACACCCT CCACTACAAT GAACTGCGTG 300
TCCGAGAGACC GCGCGGAGTC CTCTTTCTAT GAATAGAACC GAATCTCCTC GTGGCTTAAT 360
CAAAGCCACC GTACGTGAAC AAGACCGAGG CCGAACCGTT TATAAAAAGA TTGCCCAGTT 420
CCTCTCCCTC ATTGAGAAG AGCAGGGCGG GCGCTGGTGC TCAAGCAACT TGAGCCTGCA 480
CAGATTGAGG CGGTGGTTGC CGAGCTCCTG AACTCAAAC CCCTCAGTCC AGAAGAAGCG 540
CGTGAGATCC TACGGGAGTT TTCTGCCCTC TGC GCTCGTG TGTGCGCTGT TACCGGTGGA 600
CTGCGTGCTG CGCATCGAT 619

(2) INFORMATION FOR SEQ ID NO: 632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

ATCCAATAGC AGGAGCCAGG AGCCAGGTGC TTTTCCTGGT CTCCCATGGG GTGCAGGGCC	60
CAAGCACCTG GGCCATCCTC CACTGCACTC CCTGGCCATA GCAGAGAGCT GGCCTGGAAG	120
AGGGGCAACC GGGACAGAAT CCGGCGCCCC AACCAGGACT AGAACCCGGT GTGCCGGCGC	180
CGCAAGGTGG AGGATTAGCC TATTGAGCCA CGGCGCCGGC CGAAGTATTC AAGAAAAAAG	240
AGGGAAAGAT GTCTCACAGG ATGTCAAGAT TTATTCGATA GACTCATAAA TGCACAGTAA	300
GTAAAGTCAT TTGATGTTAG TGCAAATAGA CAAGTAGAGC TTGAACAGCA GGAAAGAGAA	360
GGAATAAnGn AnGnAGnGG AGGAAGGGTG GAATGTGGGT GGGAGTCAGG GAGACCTTAA	420
ATTAGGAGAG GGTGCTCCCT GGGGACAGTT TTGTGTTACA GCAGGTTAAG CTGCCACCTA	480
GGATGTCAAC AGCACATATG GtGCCAGTTC CAGTCCTGGC TGCTCCAATT CCAATCCAGC	540
TCCCTGCTAT GGCCCGGGAA ATAGAAGAAG ATGGCTCAAG TACTTGGGCT CCTGCACCCA	600
GGTGGGAGAC CTGGAAGAAG CTCCTGGCTC CGGGCTTTGG CCTGGCCCA	649

(2) INFORMATION FOR SEQ ID NO: 633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

GTGTGCCTGC TTCACGCTC CTTACGCGAT CTGAGTAATA ACTGATCTTG CCACCTGCAC	60
CGAGTTATCT ATGGTGCTAC CAACCGTATC AGCCGCCTGT TTAGCCTGTT CCTGCGCACG	120
TGCGTAAAAA TTGCCAGTGC AACCTCCTGT GCACGCTCGC GTGTCCTTTC GGTCTCATC	180
GCCGCGGTAG CCTCACTCTG GTGTTGGTTA CCGGCGTCGA GGGCGAAGGA GAAGCGGAAG	240
CCGGCGCCTG GTTCGAGGGT GAGTCGGCCC CCTACATTC ACAGCAGTTT ATCCTTGTTT	300
TGATTGTTTG CGTCCTTCTG TGGCACCGAT GAGGTATCCG TCTTCTAGCG TAACATTGGC	360
TGGGCAAGCT CTACCGTGGC ACAGAGGGTG TCCTGGCAnG CGCATACATT AGCTTCAAGT	420
CTGCCCCAAA GCCATACTTT ACTGTGCGTG GGGTCAGTAC TATCCCAGGG CACCGTTAGA	480
GGCAAAGGAG AGAAACCCCA CATCAAGGCT GACCCCACTG GCCCCCAATG TCCTGTGCCC	540
GATACCCAAC CTTGCCGCCT AAACCCCCAA ACCCGGCGC ATAATGTAAC GCATCCTCCT	600

GGTATGCGGT G

611

(2) INFORMATION FOR SEQ ID NO: 634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

CGGTATGGCG TTGATCTCTT CGGTCTGGT GTTTTAGCCC TTCGGGGGAA TTACGTGTGA	60
GTGTTCTTTC CGTTCCGCT GCGTTCGGTG TGTGGTAGT GCTGCTGGTG CTTTCCATGT	120
TGTCTCTGCG TGCGGAAACA GCGTCTGTG CGCTAAATAC CTTAAGACTT CGCTACCTGT	180
ACGAAAAACG TCATGCTCGC GCTCGAGTGG CAATGCGTAT CCTTCGACGG AAAAATTCT	240
ATCTTGCTGC TGTGGTTATC GGGAACACCC TGGCGAGCAG TGC GTTGTCT GCAGTCATTG	300
CGCTTTTTCG ACGTGCCCTC TTTGGCATCC ACGCATGGAG nTGGAGCATC GGTGCAGGAA	360
CGGTGGCTTA CACTTCTTTT TGGAGAAATT ATTCCGAATC ACTTGCCTTG TGCCGGCCGA	420
ACGCATGnCA CTGCATACTG CGCGATTCTT GCAGTGGAGC GCTTTGATGC TTACTCCTTT	480
TGTACAGGTG TTCTGTATGG GCGCGGATGC GCTCTTGCGT CTTGCGCGTG TCGGTGCCAn	540
ACTCCCTCGC TGCGTGTAG GGATGACGAC CTGCACACCG T	581

(2) INFORMATION FOR SEQ ID NO: 635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

ATTAGGTGGG AGACAGAGAA GCTTGGCCGT CAGTTnAGGC GGAGTCAACA GTGAAATACC	60
ACCCTTGGTA CGTCAGGTTT CTAACCTTTG GCCGTGGATC CGGCAAAGGG ACCGTGGTAG	120
GTGGGCGGTT TGA CTGGGGC GGTGCGCTCC TAAAAGGTAA CGGAGGTGCG CGAAGGTCTC	180
CTCACACCGG TTGGAAATCG GTGCGGAGT GTAAAGGCAC AAGGAGGCTT AACTGCGAGA	240
CCGACAGtCG AGCAGATACG AAAGTAGGTC TTAGTGATCT GGCGGTAcGT GTGGAAGCGC	300
CGTCACTTAA CGGATAAAAG GTACTCCGGG GATAACAGGC TGATTTTCCC CAAGAGTTCA	360

1085

CATCGACGGG AAAGTTTGGC ACCTCGATGT CGGCTCATCG CATCCTGGGG CTGAAGCAGG	420
TCCCAAGGGT TTGGCTGTTC GCCAATTAAA GCGGTACGTG AGCTGGGTTC AGAACGTCGC	480
GAGACAGTTC GGTCCCTATC TGCTATGGGC GTTGGATATG TGAGAGGAGC TGCTTTTAGT	540
ACGAGAGGAC CGAAGTGGAC GAACCTCTGG TGTACCAGTT ATCCTGCCAA GGTACGTGCT	600
GGGTAGCTAT GTTCGGAAGG GATAACCGCT GAAGGCATCT AAGTGGGAAG CCCGCCTCAA	660
GATTACATAT CCCTGAAGGT TGACCTTCCT GAAGACTCCT GCACACTACA AGGTCGATAG	720
GCTGGAGGTC TACGTACCGT AAGTATTAAG CCGACCAGTA CTAATAAGTC GTGAGGCTGA	780
CCATATTATC ATCCTTCTCC TTCACCCTAC CCCTTTGGGT AAAATATTTC GCCTGGTTGC	840
CAGGTGGAGA GGTCATACCC GTTCCC	866

(2) INFORMATION FOR SEQ ID NO: 636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

AGGAGnAnAA GCGGACAGG TATCCGGTTA AGCGGCAGGG TCGGAACAGG AGAGCGCACG	60
AGGGAGCTTC CAGGGGAAA CGCCAGGGGT ATGCGGTCAC CGGGGTTTCG ATCACGTCCT	120
TTGATGCGGA CGGGGTTGCG CACTTCATTT CAAGCGAGTT TGAACAGATT CCCCACGTAC	180
GGGAAGATAC CCTCGAGATT CTAAATAATT TTAAGCGTCT GCGTTTTCTC CTGCCGAGG	240
GGCAGAGTCT AGTACGTTCA CGTATGAGTT TCGCGGCGCG TGTCTTTGAC GGGGAAGGAC	300
TTTGCTAAGA AGTTTCAACT CGAGGTTCTG TCTCAAGACC TGCTCATCAT GGAAATGATG	360
GACGGTGCGC ATGTTGAAGT AGAGCTACAC GTCGAATTCG GCGGTGGGTA TGTACCTGCT	420
GAATCGCACG ATCGGTATGC CGATTTAGTT GGGGTTATCC CTGTTGACGC AATTTTTAGT	480
CCCGTGTGA GAGTCCGCTA TGATATTCAG TCTTGCCGTG TAGGTCAGCG GGGGGATTAC	540
GATCAGTTAT CCCTGAAGT GTGGACAGAT GGTACGGTGC GTCCCGAAGA CGCGATACCG	600
AGGCAGCGAA AATTATCAAG GAGCACTTTA CATTTTTGTT A	641

(2) INFORMATION FOR SEQ ID NO: 637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1086

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

ATAACCCTGA TAAATGCTTC AATAATATTG AAAAAGGAAG AGTATGAGTA TTCAACATTT	60
CCGTGTCGCC CTTATTCCTT TTTTTCGGC ATTTTGCCTT CCTGTTTTTG CTCACCCAGA	120
AACGCTGGTG AAAGTAAAAG ATGCTGAAGA TCAGTTGGGT GCACGAGTGG GTTACATCGA	180
ACTGGATCTC AACAGCGGTA AGATCCTTGA GAGTTTTCGC CCCGAAGAAC GTTTTCCAAT	240
GATGAGCACT TTAAAGTTC TGCTATGTGG CGCGGTATTA TCCCGTATTG ACGCCGGGCA	300
AGAGCAACTC GGTCGCCGCA TACACTATTC TCAGAATGAC TTGGTTGAGT ACTCACCAGT	360
CACAGAAAAG CATCTTACGG ATGGCAGACA GTAAGAGATT ATGCAGTGCT GCCATAACCA	420
GAGTGATAAC ACTGCGGCCA ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC	480
CGCTTTTTGC ACAACAGGGG GATCATGTAA CTCGCCTGAT CGTTGGGAAC CGGAGC	536

(2) INFORMATION FOR SEQ ID NO: 638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

CGTCCACTAC ACGTCTCTGA CCGGACCCCA AGCCCCAGCC GCAGCCAACA TCAACTTCCC	60
GGTATGGGGA TGCCTCACGC ACATCGCAGG CCAGCAATGT ATTTCAGGGA GTATTTCTCA	120
ACATGGCCAT GACCGCACAC GACTGCGCCA CCTCGTGGGG CGTAAGAAAG ACGGAGCGCA	180
GGGCACCGTA GGCGCGGACT GCGTGAATGT GGAGGCTCGT TTAGCTTCTC AGACGTGTCTG	240
GGGGCATTGC ATCCGATGGT GGCGCCATCA AGCAGGGAAG TGCGCACTGG GAGGGCAAAG	300
ACAGCAAGGG CGTCGTTCCA AGCAGGAGCA AACCACAGCA CGTACGGCGG TAGAACAAAA	360
AAGCTGCTGC TGCAGCCCCT GCTCCTGGTA CGAATGGAGC ACAAGAACAG GACACGCGCG	420
CACTCCCTTT CACACAAAAA ACCTCTTCCA CGCCCAGCC CGAGCCGGAG CCGCATGCCA	480
GCCGGCAGCC GACGAnTTTT ATAGGACGCA GGCCTACATG CCTGTCCATT AnAAATCTAA	540
AAAGCCCACG CCCGAGCCCC AACGGAGATC CAATTTCCCG	580

(2) INFORMATION FOR SEQ ID NO: 639:

1087

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

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TTGTATTTCGG TTCTTGCGT TGTGTGGTGC TACAACGCA TGTGCGCAGA ATCGTACGTG      60
TTCGGTTTGA GTTTCAAGGA TAGTAGGGAA GCGCGCGTGG CATACCCTTT TCTGGTAGGA      120
TTGGAACCTCA TGTTCCTACT TGTGTGCTCG GCCCTATGTG CAGGTTTACA AAGCGCGTTG      180
TCGTCGGTGA ACCAAGACGA TGAACGTAAG CTTAAGCGGC ACAGTACACG TTGTACACAA      240
CGCTTATGCT GGCTTCTGGC CCGGCGCGAA CAGCTGATTA CCACAGTTAT TGTGCAAAAC      300
ACTGCACTGA ATATGGTGCT CTCTAGCGTG GTGACGTTAG GCTCTATGGA GTTGTGGGGT      360
GCACAGTnCG GTGTGGAAGG CACTGGTTGC GGTGACGTGC GTGATTATTC TTGTGGAGAA      420
ATGTTCCCGA AGGCGCTGGG TGCACGGTAC TCACTGGGAT TCTTGATGTG GATTGCGCCT      480
TTTTTGTAAT TGAGTTACTG GTTGCTGTAC CCCTGGCGCG TGTGTGTCGT CAGCATTGAT      540
GCATGTGCTG GAGGGTATTT TTTGCCGCG TCATACGACG TGTCTTTCGC GAGAAGAAAT      600
TAAAACGCTT ATTGCAGTTG                                     620

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(2) INFORMATION FOR SEQ ID NO: 640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

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GGGCCAGTGC GTGGATTCTT CTGGAACGCA ATGCCCCACT GGAGCTGGGC TGTGCCACTG      60
ACCTGCGGAG TGAGTACGCC TGCATAACCA GAAGCAGCAC ATACCATGCC CGCAAGnGnC      120
CCCCGACTTG CATCACCTGC CTGCCCCACTC ACTCCCCCTC CTCTCACTTC nACCTCACCC      180
CCCCCACCCG TCTAGCCGCG TGTGACTACC AGGAGAGGGT GACGCCGCAC ACGATGCGGC      240
CGATTCCCTG GGTGAGGCAC TCGGACACCA GCAGGTACGG GAACATCAGA GAGCATACCC      300
TGTTCCCAAT CAAGGGAGAA TACCGTCTTC TCTATGAGAC TGGCTGAAAT ACCAGCACGC      360
AGCTGTGCAC AGTACTCCTT GGTAGATAG GTAGCTCCTA CTGCTCCACC TGCAGCAGGG      420

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GCATTCAGGT GTGACACGGT TGGTAGAGGC ATGGACCGTA ACGCTTGGCT TCACCCAGCC	480
GTAATCCTGn CACCGGGATG CGATAGTACA CCACGCCCTTC CCCACCACCG GCAGGCCAAT	540
GTGCCCTGAG GAACCGCCGG AAAGGAGAGG GTTCCCGTTA TTATTTTGT ACAGGTCATG	600
GGTGAnGGG ATGTACACGC GTGTTTCAAC GCCGGCGTCC AGGCCGGTGA GCAAGTGGGT	660
GTAAGGTCA CCGCTCTTAG TTTGAGCTT nAGGAATCCG GCAAAGTCGC	710

(2) INFORMATION FOR SEQ ID NO: 641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

CAGGTATCCG TACGCCACAT CCCCCTCAAT GCCCnCGGTT TCATTACCCC TGAAnCTGTA	60
CGTGCAAGCG TCAGTCCCCG TACCACGCTA GTTGCGTGAC GCCGTACATA GTGAAACCGG	120
CCGCCATCCA nCCGCTCCnn GnGATTGCGC ACGTGCTTGC ACATACAGGC ACACGCGGAC	180
GCTCTATCCA GCTCCACGTA GACGCCGCAC AGGCCTTTGG GAAAATACCG CTCAATCTGT	240
ATATGGACCT TCCGCGCATA GAGGAACATG CACAGGAAAA CAACGCGCCA CAGACACCAC	300
CGGGCTACCC CGCACCCACT GnACAACGCG CGCTTACCTA CTCGGTAGCA ATCAGTGGCC	360
ACAAAATAGG CGCACCACGG GGTATTGGGC TACTGTGCGC ACACCGTTCA TTTACCCCCT	420
TTGTCTGGG AGGCGGACAG GAAnAAGAGn GCCGCCCGG AACTGAGAAC TTGCAGGTGC	480
GCTCGCGCTC GCnGCTTGCG TGTGCGAAAG CGCCTTCTTC CGTACTCTAC ATACCACTCC	540
GGAnGGCCCT ACACCCGCAT TACGAAGCCC ACAG	574

(2) INFORMATION FOR SEQ ID NO: 642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

TATTTGTTTA TTTTCTAAA TACATTCAA TATGTATCCG CTCATGAGAC AATAACCCTG	60
GATAAATGCT TCAATAATAT TGAAAAAGGA AGAGTATGAG TATTCAACAT TTCCGTGTCG	120

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CCCTTATTCC CTTTTTTGCG GCATTTTGCC TTCCTGTTTT TGCTCACCCA GAAACGCTGG 180
 TGAAAGTAAA AGATGCTGAA GATCAGTTGG GTGCACGAGT GGGTTACATC GAACTGGATC 240
 TCAACAGCGG TAAGATCCTT GAGAGTTTTC GCCCCGAAGA ACGTTTTCCA ATGATGAGCA 300
 CTTTTAAAGT TCTGCTATGT GCGCGGTAT TATCCCGTAT TGACGCCGGG CAAGAGCAAn 360
 TCGTGCGCGG nCATACACTA TTCTCAGAAT GACTGGTTGA GTACTACCA GTTCACAGAA 420
 AAGCATTTAC GGGnGGACAG ACATAAGAGA ATATGCAGTG CTGCCATAAC CAGAGTGATA 480
 AACTGCGGn CCAnCTTACT TCTGACAACG ATCGGAGGAC CGAAGAGCTA ACCGCTTTTT 540
 GCACAACAGG GGGATCAGTA A 561

(2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

CCTTATTCCCT CCATTCTAAT CACACACGTG CATGCACCAA GAGGACAGCG CCGTGCTATC 60
 TTCCAGAAA GGAGGATGAA AACACGTGAA AACCATTCTC ATACTGGGTG CAGGAACCAT 120
 GCAAGCCCCT GCACTTCGCG CACACGGGAG CTGGGCTGT GGGTGTGCGC GGTAGATGGG 180
 AATCCGCATG CACCGTGCGC GGCACCTGCA GACGAGTTTA CCCCATCGA TTTGGCCGAT 240
 AGCGCCGCGC TCGTCGCTCA CGCGCGCGCA ATTGCGCGCG ACGACGGCTT GGATGCTGTG 300
 TTCACGCGG CAACAGACTT TTCCGTTTCC GTGCTGCGG TCGCCGAGGC CTGTGCACTC 360
 CCCGGGCCAC CGATTGGAGG CAACCAAAAA CGCTACGGAT AAAACGCGCA TGGTGGCCTG 420
 nCTTCACAG CGCCCGACTG CGCTGCCCCC GCTTCACGTT CCTTGAGCCT GACTCGTTTCG 480
 CTTGGGGACA CACCGCCTGG GGCATGCCCC ACTGTGTTCC CACCTGCATA GCGCTGGACT 540
 CTCGTTTCCT CTCGTCGTAA AACCGACAGA CAAACATGGG AGCCCGCGGC TGCACGCTCG 600
 CGCAATGCAA GGATACCCTC 620

(2) INFORMATION FOR SEQ ID NO: 644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

TTCCCAGAAA GGAGGATGAA AACACGTGAA AACCATTCTC ATACTGGGTG CAGGAACCAT	60
GCAAGCCCCT GCACTTCGCG CnACGGGGAG CTTGGGCTGT GGGTGTGCGC GGTAGATGGG	120
AATCCGCATG CACCGTGC GC GCACTTGCA GACGAGTTTA CCCCAATCGA TTTGGCCGAT	180
AGCGCCGCGC TCGTCGCTCA CGCGCGCGCA ATTCCGnCCC GnCGGCTTGG ATGCTGTGTT	240
CACCGCGGCA ACAGACTTTT CCGTTTCCGT CGCTGCCGTC GCCGAGGCCT GTGCACTCCC	300
CGGCCACCGA TTGGAGGCAA CCAAAAACGC TACGGATAAA ACGCGCATGG TGnCTTGCTT	360
CACACGCGCC CGACTGCGCT GCGCGCGCTT CACGTTCCCTT GAGCCTGACT CGTTCGCCTG	420
GGACACACCG CCTGGGCATG CCCGACTGTG TTCCCACCTG CATAGCGCTG GACTCTCGTT	480
TCCTCTCGTC GTAAAACCGA CAGACAACAT GGGAGCCCGC GGCTGCA	527

(2) INFORMATION FOR SEQ ID NO: 645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:

TGTTCGGTGA TTCCTGGTGG CATCATGATA TTGGGAAGGT TCTGCACGAG TTTCCCCTCC	60
ACCCGTCTAA ACACTTCCCT TGCTTTGAGG ATAGCTCTCT CTTGGGTCTG AGCATGTGCG	120
TTACTCTGGT GTTGGTTACC GCGCTCGAGG GCGAAGGAGA AGCGGAAGCC GCGCCTGGT	180
TCGAGGGTGA GTCGGCCTCC TACTCCCCAC AGGAGTGCTG TTTtGTTTTT GTTCTTGGAG	240
TCTTCGGTAC CCTTAACGTA tTCTGGTCCA GTGTGGCATT CCCTGCCAGC TCCAACGTAA	300
GCAGCCGCTG ACGGTCGACG CCATAGGAAA GCGTTGCATC GGCCCCGAAG CCATACTTGC	360
TGTGCGTGGT GTCAGTACTA TCCCAGGCAC CATTGGAAAG GAAGGAGAGG AAACCGATGT	420
CCACATCTAC TCCGCTGTTT CCCACATTGT GGGCCTGGTA GCCGAGTTTT GCGCCGAGC	480
CGGAGAAACC AGGGGCATAG CGAGTGTCTT TTTCTGAATA GGCACGGGTG ACAAAGGGkT	540
TCCACAGCTG GGCAAAGTTA ACCACACAGG GAAGnACTGG TACCCACTGT CAGTAGGGCC	600
CCATAACAGT GnCAGGGTTG CCTGGAAGGA AGCGGTAGGT TTGGTAAAGG ACAGGGCCGT	660
TGAGCTTTTA GAAGACGCAA GCTCTACTGC CAGGTCCTTC AGCTGCAGCT GTGCCCACAC	720

CCCTGAGCGT GCCTCCCCCTC GCGGGGT

747

(2) INFORMATION FOR SEQ ID NO: 646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

GTGTATGTTG CCGGGTGTGG CGGCGCGTGT TTCTCTCTCC CCCAAGCTCG GGGTGACGG	60
GGACGCACGC GCGGTTCTG ACCTGTGGGG CATCTGCATA CAAGCTCCCA CAATGCCAGA	120
TACAGAGAAC CAGGCGCCTC CGCGCTATGC CCGGAGACAC CGTTGGTGGG GCTGGACGTG	180
GCGTTCCGTG CGGAAAATGG CTTCCTGCTC CAACTGACGG TGGACGCGGC ACTCACGCGT	240
TTAATGTTCT GCGGCCGGTG TTTGGCCGGT TATTCGTTCA GACCGGGGA AGGTAGTACG	300
CATCTGTCGG TAGCGGCGGG TTTTGTAGTGC ACCGCGCTCA TCTACGATAG CCAGCACTTT	360
CTTTCGGTTC TTGGGCAGGG CTTACTGCAG CCGAGCAGCT cGTCTTATTC AGCCGGTAAC	420
TGGrCACCGCC CACGTTcATg CTTGGCGTGC TAACGTGCAC TGCCAAGGAG gTAGGCGCCA	480
TACACGAaG aGTCGgCGTA TTAAAGGGGT CTGTCCAGAA CTATGCGGTG CCGGTGCAGC	540
TGGGGGTACA GCACTATTTT AGCGCGCACT GGGGGATAGA CGCGACGGCT ACCGTTTCGT	600
TTGGCATTGA CACCAAGCTG GCTAAGTTCC GnATCCCGTA TACGTTGCGC TTTGGCCCCG	660
TCTTCCGCAC CTAGGGGACG GCGCTGGGAG GAAAGAGTCC TGCCGGAAGG CGCCTGCGGC	720
GGGTAGTAGC TACCAGGAGA GGGTGACGCG CACACGATGC GGCCGnCCCC CCCCCCCCC	780
CCCTCGGACA CCAGCAGGTA CGGGACATCA GAGAGCATAC CCTGTTCCCA ATCAAGGGAG	840
AATACCGTCT TCTCTATGAG ACTGGCTGAA ATACCAGCAC GCAGCTGTGC ACAGTA	896

(2) INFORMATION FOR SEQ ID NO: 647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

TATCCAAGTT CTGTTTGTGG GCTGCCTCGC GGTAGTCAAC AATACCAGAA ACGCTAAAGC	60
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CCTGCGTGCG CAAAGCGCTT CTCCAAAAGC TGCATAGTGC GATCGAAGGG GTAGCGGCTG	120
GTGATCGTCA TACGCACCCC CGGCCGCGTG TTGGAGGTTG ACCCGGCTGC GCTTGAAGTG	180
CAGGCAACAA GCCCTCCTAA AAGGAGCACT CCCAGGGAAG CAACCTTTCC CCACACGCGC	240
CACCTGTGAT GGCACAAACG TCTACACACC CCGCTACCT CCGCTGCGTG TCATGCCCCG	300
CCAGATATGC GCCGGCGCAA AAATTCGCCC CTTCGGAAAG AAAAGAACCA TACATCCCTA	360
CCAAATCAAG CGACATGCCC CTACGAATTG CCAACGCTCC GTCACGTTCT TCTCTATCAC	420
TACATTGCTG TTCTCTTGTA GCTTGCCTTG CTCCCAGCTC AGCCGAATCT CCACCTTCTC	480
TAACGGACTG ACCACTACCC CACACTCGTA ATACCACAA TATTCCTTGC TCCACTTCGT	540
AGCAGGAGCA GCAGGGGGCG TGGCCTTTTT GTTCGTACCG CCGT	584

(2) INFORMATION FOR SEQ ID NO: 648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

CACGTCTTCA nnCCCACCGG TAACCCCCAA CGCAGCGTGT GGCCAGTGCT GCACCGGGCG	60
TTCTTGCCCT GTTCCCCCGG CAGAATCAGA TGCGTCTCCC GTGGACCTGC CAACCGAAAA	120
TAGAnATGGC GATACACCCG GCGCTGTCCC CTCAGGGCGC GCGCCTGTCT CTCCCACCGC	180
ACCCGGACAC CGCTTTGGGA ACAACGCCAT AATTGCCCCT GnATCCATAC CCGCGTCCTG	240
GTGCACAGAC GCACCTGTAT CTGCCGGAAG GTGCACGCGA TGCGCGGTGT CTTCCACAGA	300
AACCTGATTC CCCTCCCACA AGAGAACTGA GTTTGACTGA CCCCACCCAG GAGCGGACTG	360
CTCATGCGGC GCATCCTGCG GTTCTACAGC TAGCTGCTGG CAGGCAACnA GAGCTGCACG	420
nAGTTACTTG CCACGGnnAA AAACGCGGCA CTCCAGGCGT GnATAACGCG CTTCTGGCT	480
TCATTTTCCT TTGGGCACGA TGTAATCGTA AATGTGCGCG CTTAATCCTG nnGCAACTGC	540
TGCAAGCGTG GCCACGCACT GG	562

(2) INFORMATION FOR SEQ ID NO: 649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

CGGATACCCC GGAGAAATGC ACTTGAGTTA TTTGATGAAG CGTACGAGAA ACGGTATTTTC	60
TCTCGGATTA TTGGCACAAA TGCGGTGTTC CACACACAGC TTTCGCACAA GCAGTGGTAT	120
ACTGAAACCG ATGTGTCAGG GTTGTTCGCG CGCGTCATCG CnAATnTCAT CATAATCAAT	180
CGTTGAGCAG TCTCTTGAT GATCGCAGTA TCATCGAGCG ACTCCTACAC GCTCGCTnGT	240
CCGTTGCGGG GACACCGCGC GCATAGGGTA GCGTCGCAAC GGACATGGGT TCGGGGATCT	300
TTGTGCGGGA CATCGGTACG TCTTCCCTAA AAGCGCGAT TATTCCCAA GATGGAAAGG	360
TGTTACAGTA CCAGCGCGTG TTCTTCTCTC AGCCGGTGAA GGCCAGGAT TGGGTGCGTT	420
CATTTTTTAC GGTGTTTGAG CGGTGCGTG CCGTGCATCA CGTTATTGCC ATTACTATTT	480
CGGCAATGG ACCGAGCGTC GTTGCCGTGC ACAAGAAGAG TCATGCCGAG GATC	534

(2) INFORMATION FOR SEQ ID NO: 650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:

GGGAGnAGTG ATACGCCTAT TTTTATAGGT TAATGTCATG ATAATAATGG TTTCTTAGAC	60
GTCAGGTGGC ACTTTTCGGG GAAATGTGCG CGGAACCCCT ATTTGTTTAT TTTTCTAAAT	120
ACATTCAAAT ATGTATCCGC TCATGAGACA ATAACCCTGA TAAATGCTTC AATAATATTG	180
AAAAAGGAAG AGTATGAGTA TTCAACATTT CCGTGTCGCC CTTATTCCCT TTTTnGGC	240
ATTTGTCCTT CCTGTTTTTG CTCACCCAGA AACGCTGGTG AAAGTAAAAG ATGCTGAAGA	300
TCAGTTGGGT GCACGAGTGG GTTACATCGA ACTGGATCTC AACAGCGGTA AGATCCTGAG	360
AGTTTTCGCC CCGAAGAACG TTTTCCAATG AnGAGnACTT TAAAGTCTG CTAGTGGACG	420
CGGTATTATC CCGTATGACG CCGGGCAAGA GCAACTCGTC GCCGGCATACT ACTAATTCTC	480
AGAATGGACT GGTGAGTA CTCACCAGTC CAnCAGAAAA GCCATCTTAC GGATG	535

(2) INFORMATION FOR SEQ ID NO: 651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:

ACGCTTACCG AACGCTCCCC TCCAACGCGC TCAAATACTC CGTCTTGGAG TACGCGGAGG	60
AGCTTCGGTT GCAGTTCCAG GGGGAGATCT CCGACCTCAT CGAGAAAAG GGTGCCACCG	120
TGAGCCAGTT CAAATCTTCC CCGATGGGTG CCGACCGCAC CTGAGAAGGC ACCTTTTTCA	180
TGTCCGAATA ATTCGCTTTC TGCAAGCTAT GGACGAGTGC TGAGCAATTG ACGGGGACGA	240
AGGCTTGTCG CTGCGGGTGG AAAGTTGGTG AACGGTTCGC GCAACAAGCT CCTTTCAGT	300
GCCGGTTTCT CCACAAACAA GGACAGGGAG GTCAGAGGCT GCTACGAGCT TTATAGCATC	360
GAGTGTGCGT GTCCAAGCAG GAGAGGTTCC GATCATATTT TTAAATGCAG TGATTGGGGA	420
GCTAAGAGCG CATTTCGTTC GGTCAAAGA GCGTGACTCT TTGACTCAGT GTCTCGGACG	480
CGTCGGTCTG GGCTACTGCG AGCGAGATAA GTTTAGAAAG AGTAGTAATG AAGCGTACAA	540
CGTCTGGGGT AAAC	555

(2) INFORMATION FOR SEQ ID NO: 652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652:

AAAAACATAG CCATCTGCAA ATCAGTAATG AGACGTATAG GTGGTGACAC TGCCCGGTGC	60
TGGAAGGTTA AGAGGAGAGG TTCGTGGTAA CACAACGCTT TGAATTGAAG CCCAGTAAA	120
CGGCGGCCGT AACTATAACG GTCCTAAGGT AGCGAAATTC CTTGTCGGGT AAGTTCCGAC	180
CCGCACGAAT GGTGTAACGA CTCTGGACAC TGTCTCGACG CGAGACTCGG TGAAATTTAT	240
GTACCGGTAA AGAAGCCGGT TACCCATAGT TAGACGGAAA GACCCCGTGA ACCTTCACCG	300
TAGCTTACTA TTGGAAGTTG GTTTACCATG TGTAAGTATAG GTGGGAGACA GAGAAGCTTG	360
GCCGTCAGTT AGGCGGAGTC AACAGTGAAA TACCACCCTT GGTACGTCAG GTTCTAACC	420
TTTGGCCGTG GATCCGGCAA AGGGACCGTG GTAGGTGGGC GGTTCGACTG GGGCGGTCGC	480
CTCCTAAAAG GTAACGGGAn GTnCGCGAA	509

(2) INFORMATION FOR SEQ ID NO: 653:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 499 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:

ACGCCCAGCG CCACCGCACT CATAGTGCCG nTGTACACGC GCATGnCGTG GGTCCATGTT	60
AGCGCCGATG TGAAACCACA TGGAGCCACC GATGACGTTT TCACCTTCAn TCGGGGAGAA	120
GCGGCCCCGTG AGCAAGTTCA TGCCGTTGAA CTGGGCAGAA CTAGCGATGC GgTCTACCT	180
CTGCCACAAG CTGCGAAACT TCCACCTGGA TCTGCATGCG GTCTTCAGCA GAGTAGATGC	240
CGTTTGCCGC TTGAATTGCA AGCTCTCGGA TACGCTGCAT GATGTCGGTG GTTTCTTGCA	300
GATAGGCTTC GGTAACCTGA ATGAAGTTCA CACCGTTTGA GGCATTGGTG GATGCCTGGT	360
TTAGGCCGCG GATTTGGCTG CGCATTTTTT CTGAGACAGC CAAACCAGAA GCGTCATCCC	420
CTGCGCGGnT GATGCGGTAC CGGATGAAAG CTTCTCGATG CCCTTTCCAA CCTGGACATT	480
GgGTGCCCCG AGTGTGCGT	499

(2) INFORMATION FOR SEQ ID NO: 654:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 636 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

TGGGGCGACG GCGGTACAA TGTATTGGT AAGCGGTGC TGCCTGCGCT GCGGTCCTGG	60
CATTTTGATT TTGCCGATT CCTCAAATC GAAACCAAAA GCGGTGACCC CTACACCCAC	120
CTGCTCACC GCTGAACGC CGGCGTCGAA GCACGCGTGT ACATCCCCCT CACCTACATC	180
CGTTACAGAA ATAACGGAGG GTACGAACTG AATGGAGCTG TGCCCCCTGG GACTATCAAT	240
ATGCCAATTT TGGGGAAGGC GTGGTGACG TATCGCATCC CCCTCGGTTC CCACGCCTGG	300
CTTACACCGC ATACATCCGT GCTCGGCACA ACCAATCGCT TTAACGTTAT TAACCCGCG	360
TACACCCTGT TGAATGAACG AGCGCTCCAG TACCAGGTGG GACTGACGTT CAGTCCCTTC	420
GAGAAGGTGG AGCTCAGCGC CCAGTGGGAA CAGGGGGTGC TTGCTGACGC TCCTTACATG	480
GGTATTGCCG AGAGTATGTG GTCTGAGCGT TACTTTGGCA CGTTTATCTG TGGGGTGAAG	540

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GTGGTTTGGT GAGGGGTTGT CGTGTGGGCC AGAGAACGGG TACGGTGGGG GTGCGCGTTT 600
TCCCCGTGGG GCTGTGCGCG CTCAGTTTAC AGGCGA 636

(2) INFORMATION FOR SEQ ID NO: 655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

ACAAGATGCC GCAAATCTTA AGGCTCGTTT AGAGGCTCAG CCTGTGGTTA TTGCCATGCC 60
CGCCGGTACC AACGGTAAGT TGTACGGCGC TGTCACGAGT CATACCGTTG CAGAACAAC 120
TGCGTGCATG GGATTTGAGG TTGAGCGCAA CnAGTGGAGG TCCCTGGTCT TACTCTGAAA 180
TGTGTGGGGA ACTATCACGT CACTATAAGA CTATACGAGG AAATATGTGC TGTGTTCCT 240
GTCACCATCA AAAACCAAAG CGAAGGAnCA GTGTGAGTGA GTAGACCGTT TGCGGAAGTA 300
TCTCTCTGCA CGGAGTATGT GCTGTTCGTT TTTAGTTGTG CAAAGAACTG TGCCACTTTG 360
GGGCTGGATC CACGGAAGGG AGACAGTTCT GGCAGTTGGG CCTCAACCCT TGCCTCGTTA 420
GAGGTTTCCA CGGAGAnGGG GGGGACTGTC TTTCACCACC TTCCCTCCTC TGAGTATTCC 480
TCGGAGGAGG TTCTGTGCCG GGCATGCCTA ATC 513

(2) INFORMATION FOR SEQ ID NO: 656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:

CGCGCACGGT GGTGACTGAC CGGACTCTCG TGCGAAnGAG AGTAGGAGTC TAAAATCTTA 60
TCAGGGGCTC CGGGTGGGAC TCCGGCTGCC AGGGCTCGGG CTTGGGCGTG GACGGGCACG 120
CAACCCATAA GATGTTGGCT GGGGGTTGGG CTGGGGGAAA TAGACGTGCG GCGTGCCTTG 180
GGGCGATACC CACAATATCC TGCCTTCCAC TTCGTAGGAG CAGCATCGTT TTTCTTGTTT 240
GTACCGCGCC TGTGTGCGTT TGTGCGCGCA nGTnCCCTGC TGCTGGGGCG CCCGTGTTTG 300
ACTTGCCCTC CCAGTCGGTG TGAGGCAGGC CGCGTCTATC CCTCAGTGCG CATGTCCTCC 360

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CTGCTTGAGG GGTGGGCGC CACCATTTTC ATATGCAATG CCCAGATGC AGTCGTCCTT	420
CTGCATGGGT GTGGTGAGAA AGACACCCTG AAATACATTG CTCTACTTCG TACCAGGAAC	480
TGCAGCAGCA GGGGGAACAG GGACACCTGG GTGAAAAGAC TGCACCATGC TAGGATGGGG	540
AATGGATATG TCCAAAAGTG TGA	563

(2) INFORMATION FOR SEQ ID NO: 657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:

GAACCTACT CATATATACT TTAGATTGAT TTAAACTTC ATTTTAAATT TAAAAGGATC	60
TAGGTGAAGA TCCTTTTGA TAATCTCATG ACCAAATCC CTTAACGTGA GTATnCGTTC	120
CACTGAnCGT CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTCTG	180
CGCGTAATCT GCTGCTTGCA AACAAAAA CCACCGCTAC CAGCGGTGTT TGTTTGCCGG	240
ATCAAGAGCT ACCAACTCTT TnnCCGAAGT AACTGGCTTC AGCAGAGCGC AGATACCAA	300
TACTGTnCTT CTAGTGTAGC CGTAGTTAGG CCACCACTTC AAGAACTCTG nAGCACCGCC	360
TACATACCTC GnTCTGTCTAA TCCTGTTACC AGTGGCTGCT GCCAGTGGCG ATAAGTCGTG	420
TCTTACCGGG TTGGACTCAA GACGATAGTA ACCGGATAAG GCGCAnGGAT CGGGCTGAAC	480
GGGGGGTTCG TGCACACAGC CCAGCTTGGA GCGAAnGACC TACACCG	527

(2) INFORMATION FOR SEQ ID NO: 658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658:

CTGnCAGTTC CTGGTACGAA nAGAGGCAAT GTATTTTCAGG GTGTCTTTCT CACCACACCC	60
ATGCAGAAGG ACGACTGCAT CTGGGGCATT GCATATGAAA ATGGTGGCGC CCAACCCCTC	120
AAGCAGGGAG GACATGCGCA CTGAGGGATA GACGCGGCCT GCCTCACACC GACTGGGAGG	180
GCAAGTCAAA CACGGGCGCC CCAGCAGCAG GGACGCGCTG CGCCACAAAC GCACACAGGC	240

1098

GCGGTACGAA CAAGAAAAAC GATGCTGCTC CTACGAATGG AAGGCAGGAT ATTGTGGGTA 300
 TCGCCCCAAC GCACGCCGCA CGTCTATTTC CCCCAGCCCA ACCCCAGCC AACATCTTAT 360
 GGGTTGCGTG CCCGTCCACG CCCAAGCCCG AGCCCTGGCA GCCGGAGTCC CACCCGGAGC 420
 CCCTGATAAG ATTTTAGACT CCTACTCTCC TTCGCACGAG AGTCCGGTCA GTCACCACCG 480
 TGC GCGTATA TTCGGGGGAG TATTTCTCAC CAATAACATG CTGCAGCACG ACTGCGCAGT 540
 CAGACGTGGG GCATAAGAAA GAGAATGCAG CGAACGTCAA TGGCACCGTG AGCGCCGGCA 600
 CGCGGGGGCA TTGCATCCGA 620

(2) INFORMATION FOR SEQ ID NO: 659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659:

CCGGTCTGCC TCCTGACGnA TCAGGTCTGC GGATGCAAGG GTCCGCGTGT TACCGTCTTT 60
 GAGAGCAGAT TTTTGGGAATG TCTCGTTTTT AATTGCGGAT TCAGGGAGTC GTTTTGCCTC 120
 TTATATGCGG CGCACCCATG CTCAAGGGTT TnGGGAACGG ATGGGTCAA TTATGGCGTT 180
 ACCTTTTCAG CTGCATGATG CGTATCCCC CAnCGTGGTG GGGAGAAGGG AGACAGCTGG 240
 TAGAGGATCT TGCCTTTGAG GTGTGTGCAG GTCTGGAGTA TCTGGAGTCT GTGACCCAGT 300
 TGCAACCGGT ATACACCGTT TCAGTGGACA nGCAAnGAT AGTCGTTnGT TGCAGCTAAG 360
 GCTGATGTCA TGGGGCGTTG TTTTGTGTTA CCAGAAATTC ATGACGCAGA ACTGACAGGA 420
 AACGCGGCGC TCCnTGTGTT GCCTGGATTT GATGCGGATA TGCAAACAnC AGCGCAACGG 480
 CGTGTCGTCT CAAGCGTGAG TTT 503

(2) INFORMATION FOR SEQ ID NO: 660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660:

ATTCAGTTCG TACCTCCGT TATTTCTGTA ACGGATGTAG GTGAGGGGGA TGTACACGCG 60

1099

TGCTTCGACG CCGGCGTTCA GGCCGGTGAG CAGGTGGGTG TAGGGGTCAC CGCTTTTGGT	120
TTTCGAGTTTG AGGAATCCGG CAAAATCAAA ATGCCAGGAC CGCAGCGCAG GCAGCACGCG	180
CTTACCAAAT ACATTGGTAC CCGCCGTCGC CCCATACAGT CCAGCCGACA CATAGGTCCA	240
CTGCGCCGTA AGCAGCGCAT CAGCATTGAA CCGGTCCAGC CGTGCACGCT CAAGCCAGGT	300
TAGCAGCATG ATAAGCACGA TGTCCGACTG ACTCGGCGCC ACAATCTCCT GTAGTCTCTG	360
CTCCGCTGCG GCCCTCTGGG GCAAGAGTTT TACCAACGCC ATTTGGATAA ACCGATCTCC	420
ACTATCAGTG GCAACCTTCG TCAGCGTAGA GACGAGCGTA CCGTCCTGCA GCGTGAGGGC	480
AAGCCCCACC CGCTCGAGAA TCGAGGACTC CGCCATCTGT CnCAGCAAAA ATTCAAGATA	540
CTTATCCTTT ACACGGTant GCTCCAACCC TGAAGGGAAT CGAAACG	587

(2) INFORMATION FOR SEQ ID NO: 661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661:

AGGAAGTAAA AAAAGACGCT GCGCTGGTAC AGGTGCGACC CCTGTTGCGC GCAnAGACGC	60
AGACGTGCGC ACACATGCTG CACGCAAAAA AATGGTACAG GCGTTGCGCC TACACATGAA	120
GGTTTGTGCG CGTGAGTTAC GATTGAAGA GGCAGCCCTC ATCCGAGACA AAATTTTGCA	180
ACTGCAAAGG CAAGACGAGC AAAACGGGGT TTGATAGGGG AGGTGGAATC GAACAGCACG	240
CGTTTTTACC ATGTCACTTT CATTCGCGAG ACAAGGGTGC CGAAGTGCGC TTCGGACCAG	300
ATGCTCTCGG CAATGCCCAT GTAAGGAGCG TCACAAGCAC GCCCTGTTCC CACTGGGCGC	360
TGAGCTCCAC CTTCTCGAAG GGA CTGAACG TCAGTCCAC CTGGTACTGG AGCGCTCGTT	420
CATTCAACAG GTTGCCCGCG GGGTTAATAA TGTTAAAGCG ATTGGTT	467

(2) INFORMATION FOR SEQ ID NO: 662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662:

1100

GCCAAAGTAT GCTGCACCCC CAGCTGCACC GGCACGCGT ATTCTGGCAA ATCCCCGTGA	60
TGCCCAATTC CTCAGACTCA GCCCTAGCAT CCTGACACTT CCGGCGCCTC AGCAGGCTCA	120
GCACTGTCTT TGAACGTAC CACCCTCCAT GTTCGAACGA ACACACCGAA CCCTCATTTG	180
GGGCCTGGAT GGTGATGTAA TGGTAGCTGT CGTAGATGAG CGCAGTGCAC TCAAAACCCG	240
CCGCTACCGA CAGATACGTA TTTACCCCCC CCCGGCCTGA ACGAATAAnC GGnCAAACAC	300
TGACCACGGA ACATCAGGCG GGTGAGCGCC GCGTTCACC GTCAGCTGGA GCAGAAAACC	360
ATTCTCCGCA GGAACGCCAC ATCGAGTCCC ACCAnCGGG TCTCCGGCGC ATAAGGGGAG	420
TAATACTCCA TCTCCGTGTC ATCGGGATCC CCATTACCTC CTTGCATCGG TCGCCTTAAT	480
ACACAAGCCC CACAAGTCAA GAACGCCACG TGGGTThCCA nAAGGCCCA	530

(2) INFORMATION FOR SEQ ID NO: 663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663:

ATTCAAAGCG TTGTGTTACC ACGGAACCTC TCCTCTTAAC CTTCCAGCAC CGGGCAGGTG	60
TCACCACCTA TACGTCTCAT TACTGATTTG CAGATGGCTA TGTTTTTGAT AAACAGTCGC	120
CTGGACCTGC TTTCTGCCAC CCTCACAAA GGCAAGGGTC ACACTTCTCC CGAGGTACG	180
TGTGTATTTT GCCGAGTTCC TTGACGCGAG TTCTCTCGAG CGCCTTAGAT TACTCATCCT	240
ACCTACCTGT GTCGGTTTGC GGTACGGTCT CTTGCAACCT AACCTTAGAC AGTATTTCCC	300
GTCGCCATGA CTACACCTGC TTCCCTTCGC TCATCGCTCC AGTCGCACTC GCACCTTACC	360
TCGAACGACG GATTTGCCTA TCGCTCTTAA AAGGCTCGGG ATACTTAGAC CAAAACCTACC	420
AATCTTTGGC CGGGCTCAAC TCACGGTCCT GCCATCGAAA TGCAAGAGGT TCGGAATATA	480
AACCGGATTC CCATCGACTA AGACCCTCGT CCTCGCCTTA AGGGGCGAnT AACCT	535

(2) INFORMATION FOR SEQ ID NO: 664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664:

GCAGTGCCAG CCGCAGCCGA CGACATCTTA TAGGACGCAG CGTACATGCC TGTCCATTAC	60
AAAGTCCTAA AAGCCCACGC CCGAGCCCCA GCCGACATCC ACTTCCCGGT GTGGGACGTC	120
CGCCCGCATC GAAGGCCAGC AATGTATTTCG AGGGAGTATT TCTCGCTAGA AACATAGCCA	180
TGCGAGAGCA CGACTGCGCA AACCTCACGG GGCATTGCAT CTGAAAAAAA TGGTGGCGCC	240
CAACCCCTCA AGCAGGGAGG ACGCGTGCAC TGGAGCTAGG CGCACCCCTT TAACACCGAC	300
TGGGAGGGCA AACCAAACGG GCAACGTTCC CAGCAGGAGT AACCCCAGC ACGTTACGGG	360
CGGTACGAAC AAGCAAGCTG GCTGCGGGTC CCCGGGCGTC GTCCCTGGTG GCGGTTCCCTG	420
GCTCTTACGA ATGGGGAGGC AGGAACAAGA CACGCGCGCA CATCCCCCTC ACACAAAAAA	480
CCTCGTTCCA CGCCCAGGCC GTACCCCAG CCCGGAGTTG ACATCTACTT CTCGGGTCGG	540
CAGTCGCCC GAGGAATCC ACACTGTTCT AGCGGGTATG CCCAAGCAGC CGGGAGCCGG	600
CAACCGGGAG TTCCAGCCCT AACCGGGAGC CGGCAnCCCC A	641

(2) INFORMATION FOR SEQ ID NO: 665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665:

TTTACACGGT ATTGCTCCAC CCTGAGGGCA TCGAACGCGC TGTCAAACCTT CTCCCGTGAG	60
CTCCCGTTG CCAGAAGCGC ATTACCTGCA TCGGCAGGCTT CCTGGTGTG GTTACCGGCG	120
TCGAGGGCGA AGGAGAAGCG GAAGCCGGCG CCTGGTTCGA GGGTGAGTCG GCCTCCTACT	180
CCCCACAGGA GTGCTGTTTT GTTTTCGTTC GTGGAGTCTT CGGTACCCTT ACGGTAGTGC	240
TGCTCCAGTG TGGCATTTCC TGCCAGCTCC AACGTAAGCA GCCGCTGACG GTCGACGCCA	300
TAGGAAAGCG TTnCATCGGC CCCGAAGCCA TACTTGCTGT GCGTGGTGTC AGTAnTATCC	360
CAGGCACCAT TGGAAAGGAA GGAGAGGAAA CCGATGTCCA CATCnACTCC GCTGTTTCCC	420
ACATTGTGGG CCTG	434

(2) INFORMATION FOR SEQ ID NO: 666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1102

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666:

GGGGGGTTTCG TGCACACAGC CCAGCTTGGA GCGAACGACC TACACCGAAC TGAGATACCT	60
ACAGCGTGAC TATGAGAAAG CGCCACGCTT CCCGAAGAGn AAAGGCGGAC AGCTCTTGCT	120
AGATGTTGCG ACACGTAACC GGTTTGTGCT TTCGGATCCT GCGCCGGCGG TTTTGTGGAA	180
TGCCTTCGCT GACTCGGGTA TTGACGTAAC GCTCCTGACC TGGACTCACA TTGAGCATTT	240
CAATGATTTG CGCAATGCTA TCTTCGTGGA TATCGACGAA TGCTTCAAAC AGGCGGGCAT	300
TGAGGTTCCC TTTCCGCATG TGGACGTACG GGTGCAGGGG GCGTGCGATG CGCCACGTGC	360
GGAAAnGGTG TGAAATGCAG GGTGAGTCTT GAnGTGCGCT TTTTCTTTGG ACATTGACAG	420
GATGGATAGA GGGACAGGGG GAAGCCGAAT GAGATGAAAG GAAAAACGGT GAGCGCTGCG	480
CTCGTAGGGn AACTCATTGC CCTAAGCGTA nGGGTGGTTG CGTGTACTCA GGTGAAGGAT	540

(2) INFORMATION FOR SEQ ID NO: 667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667:

AGCAGGTGTA TCATGGCGAC GGGAAATACT GTCTAAGGTT AGGTTGCAAG AGACCGTACC	60
GCAAACCGAC ACAGGTAGGT AGGATGAGTA ATCTAAGGCG CTCGAGAGAA CTCGCGTCAA	120
GGAACTCGGC AAAATACACA CGTAACCTCG GGAGAAGTGT GACCCTTGCC TTTGGTGAGG	180
GTGGCAGAAA GCAGGTCCAG GCGACTGTTT ATCAAAAACA TAGCCATCTG CAAATCAGTA	240
ATGAGACGTA TAGGTGGTGA CACCTGCCCC GTGCTGGAAG GTTAAGAGGA GAGGTTGCTG	300
GTAACACAAC GCTTTGAATT GAAGCCCCAG TAAACGGCGG CCGTAACAT AACGGTCCTA	360
AGTAGCGAAA TTCCTGTCGG GTAAGTTCCG ACCCGCACGA nTGGTGTAAC GACTCTGGAC	420
ACTGTCTACG ACGCG	435

(2) INFORMATION FOR SEQ ID NO: 668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1103

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668:

CCACCGCTAC CAGCGTGGTn TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG	60
TAAGTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTTCT TCTAGTGTAG CTTGTGTATT	120
AAGGCGACCG ATGCAGAGGA GGTAAGTGGG GATCCCGATG ACACGGAGAT GGAGTATTTA	180
CCTCCCCGTT ATGCGCCGGA GACGCCGCTG GTGGGACTCG ATGTGGCGTT CCGTGACGGA	240
GAATGGTTTT CTGCTCCAGC TGACGGTGGA CGCGCGCTC ACCCGCCTGA TGTTCGGTGG	300
TCAGTGTTTG GCCGGTTATT CGTTCAGGCC GGGGGGGGGT AAATACGTAT CTGTCGGTAG	360
CGGCGGGTTT TGAGTGCACT GCGCTCATCT ACGACAGCTA CCATTACATC ACCATCCAGG	420
CCCCAATGA GGGTTCGGTG TGTTCGTTTC AACATGGAGG GTGGTACGTT CCAAAGACAG	480
TGCTGAGCCT GCTGAGGCGC CGGAAGTGTC AGGATGCTAG GGCTGATCTG AGGAAT	536

(2) INFORMATION FOR SEQ ID NO: 669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669:

TGGGGCGCTG AGCTCCACCT TCTCGAnGGG ACTGAACGTC ATCCCACCTG GTACTGGAGC	60
GCTCGTTCAT TCAACAGGGT GTACGCGGGG TTAATAACGT TAAAGCGATT GGTGTGCCG	120
AGCACGGATG TATGCGGTGT AAGCCAGGCG TGGGAACCGA GGGGGATGCG ATACTGCACC	180
ACGCCTTCCC CAAAATTGGC ATATTGATAG TCCCAGGGGG CACAGCTCCA TTCAGTTCGT	240
ACCCTCCGTT ATTTCTGTAA CGGATGTAGG TGAGGGGGAT GTACACGCGT GCTTCGACGC	300
CGGCGTTCAG GCCGGTGAGC AGGTGGGTGT AGGGGTCACC GCTTTTGGTT TCGAGTTTGA	360
GGAATCCGGC AAAATCAAAA TGCCAGGACC GCAGCGCAGG CAGCACGCGC TTAC	414

(2) INFORMATION FOR SEQ ID NO: 670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670:

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GGCAACATAC ACCCGAGCAC CATCACTTTA CCCAGACGCT TCCCGCACAT ACCCCTGCAA      60
TCCCTCGCCT GTAAACTGAG CGCGCACAGC CCCACGGGGC AAAACGCGCA CCCCAGGGn     120
nACCCGTTCT CTGGCCCACA CGACAACCCC TCACCAAACC ACCTTCACCC CACAGATAAA      180
CGTGCCAAAG TAACGCTCAG ACCACATACT CTCGGCAATA CCCATGTAAG GAGCGTCAnA     240
AGTCACCCCC TGTTCCTACT GGGCGCTGAG CTCCACCTTC TCGAAGGGAC TGAACGTCAT      300
CCCACCTGGT ACTGGAGCGC TCGTTCATTC AACAGGGTGT ACGCGGGGTT AATAACGTTA      360
AAAGCGATTG GTTGTGCCGA GCACGGATGT ATGCGGTGTA AGCCAnGCGT nGGAACCGAG      420
GGGGATTCTGA TTA                                                         433

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(2) INFORMATION FOR SEQ ID NO: 671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671:

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ACCTAGGGGA CGGCGCTGGG AGGAAAGAGT CCTGCCGGAA GnGCCCTGCG GCGGGTAGTA      60
GCTACCAGGA GAGGGTGACG CCGCACACGA TGCGGCCGAT TCCCTGGGTG AGGCACTCGG      120
ACACCAGCAG GTACGGGACA TCAGAGAGCA TACCCTGTTC CCAATCAAGG GAGAATACCG      180
TCTTCTCTAT GAGACTGGCT GAAATACCAG CACGCAGCTG TGCACAGTAC TCCTTGGTTA      240
GATAGGTAGC TCCTACTGCT CCACCTGCAG CAGGGGCATT CAGGTGTGCA CGGTTGGTAG      300
AGGCATGGAC CGTAACGCTT GGCTTCACCC AGCCGTAATC CTGCACCGGG ATGCGATACT      360
AACACCACGC CTTCCCCACC ACCGGTGGAC GGATATACTC CTTTTCCTGA ATGCC           415

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(2) INFORMATION FOR SEQ ID NO: 672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672:

1105

TCGTTGGTAA GTCTCGCTAC CAACAGGGCG CTGCCCTACT ATACGACAGC CGTGTGAAG	60
CAAGCTGTTC CAGGAAAATA TACGGAGGAT CAACGCTGTG GTGCCAGCAA AAAGCGCAA	120
CGCTCACCTC TTCCCAGGAA CTGGAAAAGG CAGTGTATTC GTTGTCGTT CCCACGTTTG	180
AAAACCTGGT GTTGGGTGCA GGCGCGCTGC TGGCTCTTTT GGATATGCAT CAGATTGCGG	240
TGGACGCGCT GTTTACGGCG CAGTGGAAGT GGCTGTCTTC TGGCATATAC TTTGCCACAG	300
CACCGGCAAA CGTTTTTGGC ACCAGGGTGT TAGATAACAC CATCGCAAGC TGTGGCGACT	360
TTGCCGGATT CCTTAAGCTC GAAACTAAGA GCGGTGACCC CTACACCCAC CTGCTCACCG	420
GCCTGGACGC CGGCGTTGAA ACACGCGTGT ACATCCCCCT CACCTATGCG CTATACAAAA	480
ATAACGGGGG GACGGCTGTG CGTGGCATTC AGGAAAAGGA GTATATCCGT CCACCGGTGG	540
TGGGAAGGC GTGGTGTAGC TATCGCATCC CCGTGCAGGA TTACGGCTGG GTGAAGCCAA	600
GCGTTACGGT CCATGCCTCT ACCAACCGTG CACACCTGAA TGCCCTGCT GCA	653

(2) INFORMATION FOR SEQ ID NO: 673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673:

ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT GAGTACTCAA	60
CCAAGTCATT CTGAGAATAG TGTATGCnGC GnCCnAnTnG CTCnGCnCG GCGTCAATAC	120
GGGATAATAC CGGCCACAT AGCAGAACTT TAAAAGTGCT CATCATTGGA AAACGTTCTT	180
CGGGCGGAAA ACTCTCAAGG ATCTTACCGC TGTGAGATC CAGTTCGATG TAACCCACTC	240
GTGCACCCAA CTGATCTTCA GCATCTTTTA CTTTCACCAG CGTTTCTGGG TGAGCAAAAA	300
CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC ACGGAAATGT TGAATACTCA	360
TACTCTTCCT TTTCAATAT TATTGAAGCA TTTATCAGGG TTATTGTCTC ATGAGCCACG	420
TTACGTGCTT CGnTTTTCTC CCGCTCACGC TTATCAn	457

(2) INFORMATION FOR SEQ ID NO: 674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674:

TGATGCCGCA TAGTTAAGCC AGCCCCGACA CCCGCCAACA CCCGCTGACG CGCCCTGACG	60
GGCTTGTCTG CTCCCCGGCAT CCGCTTACAG ACAAGCTGTG ACCGTCTCCG GGAGCTGCAT	120
GTGTCAGAGG TTTTCACCGT CATCACCGAA ACGCGCGAGA CGAAAGGGCC TCGTGATACG	180
CCTATTTTTTA TAGGTTAATG TCATGATAAT AATGGTTTCT TAGACGTCAG GTGGCACTTT	240
TCGGGGAAAT GTGCGCGGAA CCCCTATTTG TTTATTTTTC TAAATACATT CAAATATGTA	300
TCCGCTCATG AGACAATAAC CCTGATAAAT GCTTCAATAA TATTGAAAAA GGAAGAGTAT	360
GAGTATCAAC ATTTCCGTGT CGCCCTATTC CCTTCGAAAT ATCTGTGAGC GGAAnTCTGC	420
GTGTTTACTC ACCTGGCAGC GACTCAACGC GCAACACCCA AGGACGAGCA GAAGATGTGC	480
GCGGCAC	487

(2) INFORMATION FOR SEQ ID NO: 675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675:

ATTCTGAGAA TAGTGATGC nGCGACCGAG TTGCTCTTGC CCGGCGTCAA TACGGGATAA	60
TACCGCGCCA CATAGCAGAA CTTTAAAAGT GTACGCTCCT ATGATTAGAC GTTCCATCGT	120
CTTCTGGTTA AAGAGACTGG AGGTGCCCTT GTGATCGGCG TGCAnGTGCT CAATCGTCTT	180
GAATATCAG TCAAGGGAGT GGAGCGGnTT TGGATCGCGG TAAGTTAGTG AGGAAAATAT	240
GCCATGTACT GGATCTGGCA GGGTGAATGC ACCGTAAGCA CCACCTATCG TTCGAATTTT	300
TTCCCAAAAn GGGnTCAGTA CTTAGATATC GGGGnAAACA CCTGGCTCTA CCCC GCGTCT	360
CTCCAAAGGA AGCCGTGGGA TGTGCAAnGG ACAGCGCTGC AAAACCCACT TGCACAGGGn	420
TGGAAGCAGC GTTCACATAT TGCGGGTGCG CATGTGCTGC AGGGCTCTTG AAAGAGCA	478

(2) INFORMATION FOR SEQ ID NO: 676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676:

AACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAnAATTA TGCAGTGCTG	60
CCATAACCAT GAGTGATTAC AGACCCGTCA CTGCTTCTCA CACACGCATC GGCAGTGCTC	120
TGCGCACGCT TTCCTGCATG ATTACGCGGT GAACAnGCAG CATTTCGGTAA AATTACCGAA	180
TCATTCCCTAG GACGGGGCCC AATACCCTCG GTGCGAAACA AATCCAGACA ATCGCGCACC	240
ACACGCAnGA AGCGTGCGAT ACTCTCTCTG TCCCCAGnGT GCATAGGACT GAGCCTACCA	300
TAAACTGCGT ACATGACGGT ACCCGATCCT TGACATCTGT CAATAGACAC TACACGAGCT	360
CTGCCCCGGG CACAGTGGA ACGAACCGAC GCGTACGCAC CTGGnAGCCG TTCGGGTAAG	420
TCTGTTAAAA nCTATACCTG TGG	443

(2) INFORMATION FOR SEQ ID NO: 677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677:

CTGCTACAGA CGTGGGGCAT AAGAAAAACG GAGCGAATGG CGACATAGGC GCAGATGCGT	60
TGTTGACGTT GGGGTATCGT TGGTTCTCGG CGGGAGGATA TTTCGCATCG AAGGCCAGCA	120
ATGTATTCGG GGGAGTATTT CTCAACATGG CCATGCGAGA GCACGACTGT GCTGCCTATA	180
TTAAGCTCGA AACCAAGGGG TCTGATCCTG ATACTTCTTT CTTGAGGGT CTTGATTTGG	240
GTGTTGATGT GCGTACGTAC ATGCCCCGTCC ATTGGAACGC CTTACCCAA GCCCGAGCCC	300
TACCCGGAGC CGACATCCAC TTCCCGGTGT ATGGAAGT CTGGGGTTCG TATCGTCATG	360
ATATGGGTGA GTATGGTTGG GTTAAAGTGT ATGCAAACTT GTACGGCGGT ACGAACAAAA	420
AAGCTGCTGC TGCAGCCCCCT GCTGCTCCTA CGAATGGAAn GGCAGAATAT GTGGGTATAC	480
GAnTGTTGGG TATGGTCATC CGTTAGAGAA GTGGAGAT	518

(2) INFORMATION FOR SEQ ID NO: 678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678:

CGAAACGGTA GCCGTCGCGT CTATCCCCCA GTGCGCGCTA AAATAGTGCT GTACCCCCAG	60
CTGCACCGGC ACCGCATAGT TCTGACAGAC CCCTTTAATA CGCCGACTCT TCGTGATATGG	120
CGCCTACCTC CTTGGCAGTG CACGTTAGCA CGCCAAGCAA TGAACGTGGG CGGTGCCAGT	180
TACCGGCTGA ATAAGACGAG CTGCTCGGCT GCAGTAAGCC CTGCCCAAGA ACCGAAAGAA	240
AGTGCTGGCT ATCGTAGATG AGCGCGGTGC ACTCAAAACC CGCCGCTACC GACAGATGCG	300
TACTACCTTC CCCCGGTCTG AACGAATAAC CGGGCCAAAC ACCGGGCCGC AGAACATTAA	360
ACGCGTGAGT GCCGCGTTCC ACCG	384

(2) INFORMATION FOR SEQ ID NO: 679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679:

CTGACGTCTA AGAAACCATT ATTATCATGA CATTAACTTA TAAAAATAGG CGTATCACGA	60
GGCCCTTTTCG TCTCGCGCGT TTCGGTGATG ACGGTGAAAA CCTCTGACAC ATGCAGCTCC	120
CGGAGACGGT CACAGCTTGT CTGTAAGCGG ATGCCGGGAA GGTAAATACT CCATCTCCGT	180
GTCATCGGGA TCCCCACTTA CCTCCTCTGC ATCGGTCGCC TTAATACACA AGCCCCACAG	240
GTCAGGACCG CCACGTGCGT CCCCATACGC CCCAGCTTG GGAGAGACAG AAATACGCGC	300
GGCCACGCAC GGCAACGCAC ACCCGAGTAG CACCACTTTA CCCAGACATT TTCTCCACAT	360
ACCTTCACTC CTCCCCGCAA TTCTTCGACA GGACCCGTTC CTCCCGGCGC CTCCCCTAGG	420
TGCGGAAGAC CGGGCCAACG CGCAACGTAT ACGGGATGCG GAACTTAGCC AGCTTGGTGT	480
CAATGCCAAA CGAAACGGTA GCCGTCGCGT CTATC	515

(2) INFORMATION FOR SEQ ID NO: 680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680:

CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC	60
TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC	120
TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA	180
GCTCAGCTG TAGGTACAGT AGGCGCGAAT AAAAATTCAA TTAAGATTAT TGGTGAGGCG	240
ACGGATAATA ACGCGCAGGC TTA CTTTGCC TACGATAGCA AGAAGTCTGG TGGTTTTACT	300
ATTTCTCATT TGCCTTTTGG AAAGCAGAAG ATCCGTAAGC CCTACCTTCA TTACGCAGGC	360
GGATTTTGTA GCGTGTCATA AGTTTACGTA CCTTGAAACC TTTGACATGC TCAAAACGCT	420
CAAGCGTGGA GGGACCTTTT TGCTGAATGC GCCGTACAGT GAGCATGAGG TGTGGCATCA	480
CATACCCATA GAAGTCCAGC GTCAGATCAT TGAAA	515

(2) INFORMATION FOR SEQ ID NO: 681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681:

TGGCAGTTTC TGTGGTCAAC GCGCTGTCGT TGTGGGTAGA AGTGACAGTG TATCGTGATG	60
GTGCTGAGTA TTATCAGAAG TTTAATGTGG GGATGCCGCT TGCTCCAGTA GAGAAGCGGG	120
GAGTGTCGGA AAAACGTGGG CACTATTATC CGCTGGCAGG CGGACCCATC CATTTTCAAA	180
GAAACGGTGG CCTATGATTT TGACGTACTC CTGACGCGTT TCGTGAACT TGCTTTTTTG	240
AATACCCATT GGGCTTGAAG ACCGTCTAGA GGGTGTCATC GATTTAATTT CGCTCAAAGC	300
CCTTTATTTT GAGGGAGAAA GTGGCGCGCA CGTGCGTGAG GCGCCCATTC CCGAACAGTA	360
TCAGGCAGAT GTGAAAAAGT ACCGGGATGA ACTCATCGAT GCGGCGTCTT GTTTTCTGAC	420
GAGCTTGCTG AGGCCTACCT TGAAGGAAGT GAGACCGATC AATTGATTCTG AGCGGCATAC	480
GTGCGGGCAn CATTCGAGAA AAGTTTGTCn CGGTTTTTTTG CGGTTCTGCG TACAAAAATA	540
AAGTATTCAG CCACTTTGGA CGCT	564

(2) INFORMATION FOR SEQ ID NO: 682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1110

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682:

ACACAGCCCA GCTTGGAGCG AACGACCTAC ACCGAACTGA GATACCTACA GCGTGACTAT	60
GAGAAAGCGC CACGCTTCCC GAAGAGnAAA GGCGGACAGG TATCCGGTAA GCGGCAGAGC	120
TGCTCTTAAC TGACTTTTCGT GCTGCGTTGG AGGATGACTT TTCTACGCCA CGTGCTCTGA	180
GCGCCTTACA AAAATTGGTG CGTGATACCT CGGTGCCGCC ATCGCTGTGT GTTTCGGCAC	240
TCCAGGTGGC GGATACAGTG CTAGGGTTAG GCATAATACA GGAAGCGACC GCATCGCTAT	300
CTGCGCAGGT TCCTGCTGGC GATACGTTGC CGCAGCGTCC TTTACCGAGT GAGGAGTGGG	360
TTGGACAGTT GGTGCGTGCG CGTGACATG CACCCAAACG CGTGATTTTC CCCGTGGCAG	420
ATGAGATCCG TC	432

(2) INFORMATION FOR SEQ ID NO: 683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683:

TGnTAACTCT GCCTTTAAAT AAATAAATAA ATACATCTTT TAAAAAATG AATGGAAAAG	60
CTCAACATCA AAAAATCCTT CCTGTGCATA TAAATAAGTG CAGGCAATAG GGGAGGGTGA	120
CATTATTCTT ACTTGATATAA AGAACTGTTT AGGCCGGCAC CGCGGCTCAC TAGGCTAATC	180
CTCCGCCTAG CGGCGCCGGC ACACCGGGT CTAGTCCCGG TTGGGGCGCC GGATTCTGTC	240
CCGGTTGCCC CTCTTCCAGG CCAGCTTTCT GCTGTGGCCA GGGAGTGCAG TGGAGGATGG	300
CCCAGGTGCT TGGGCCCTGC ACCCATGGG AGACCAGGAA AAGCACCTGG CTCCTGGCTC	360
CTGGCTCCTG GCTCCTGCCA TCGGATCAGC ACGGTGCGCC GGCCGCAGCG TGCCGGCCGC	420
GGCGGTCATT GGAGGGTGAA CCAACGGCAA AGGAAGCCCT TTCTCTCTGT CTCTCTCTCT	480
CACTGTCCAC TCTGCCTGTC AAAAAATAAA AAATTAAAAA AAAAAGTGT TAGTTTTTTG	540
TTGCATTAGT CTCATAGTAT CTTACTGGAA AnGTGTTCCA GTGTCCTAAT GGnCATTCAG	600
GGGCTGAACT TGCCATGATG GTAAATTTTT GGGATAATTC ATAAATAATG CAATTTTTCT	660
TCTCTAGAAG AATGGnnTTT CTCCAACCCC T	691

1111

(2) INFORMATION FOR SEQ ID NO: 684:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684:

TGCTGCAGTG GTTAATGAGA CGTAATCAAC ATCATCATGG CCTTGACAC ACCATGGCAT	60
CACTTCCCTG AGACAGTGCT AGCCTGGGTC TTTAAGCATG CTTTAAATCC GACAGGTCAG	120
ACTTTATATA AACTATCCCC CCCCCCTTTT TTTTTTGACA GGCAGAGTGG ACAGTGAGAG	180
AGAGAGACAG AGAGAAAGGT CTTCTTTTGC CGTTGGTTCA CCCTCCAATG GCCACCGCGG	240
CCAGCGCGCT GTGGCCAGCG CACCGCCTGA ATCCGATGGC AGGAGCCAGG AGCCAGGAGC	300
CAGGTGCTTT TCCTGGTGTC CCATGGGGTG CAGGGCCCAA GCACTTGGGC CATCCTCCAC	360
TGCACTCCCT GGCCACAGCA GAGGGCTGGC CTGGAAGAGG GGCAACCGGG ACAGAATCCG	420
GCGCCCTGAC CGGGACTAGA ACCCGGTGTG CCGGCACCGC TAGGCGGAGG ATTAGCCTAG	480
TGAGCCGCGG CGCCGGCCCC GTTTTTTCTT TAATTTAGTG CAAGGAACTC AGGTTTATTG	540
TCAGAAATGG AAATGATGGC TGATAnCTGC GTGCGT	576

(2) INFORMATION FOR SEQ ID NO: 685:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 578 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685:

CnGAGAGAAA GGTnTTCCTT TGCCGTTGGT TCACCCTCCA ATGGCCGCCG CGGCCGGCGC	60
GCTGCGGCCG GCGCACCGCG CTGATCCGAT GGCAGGAGCC AGGAGCCAGG TGCTTTTCCT	120
GGTCTCCAC GGGGTGCAGG GCCCAAGCAC CTGGGCCATC CTCCACTGCA CTCCCTGGCC	180
ACAGCAGAGG GCTGGCCTGG AAGAGGGGCA ACCGGGACAG AATCCGGCGC CCCGACCGGG	240
ACTAGAACCC GGTGTGCCGG CGCCGCTAGG GGGAGGATTA GCCTAGTGAG CCACGGCGCC	300
GGCCCATAAA ATAAATCTTT AAAAACAGTT TATTTTTAAA AAAGGTGGCT TTAATTTTCT	360
TTTATTTTGG GCAAAGCTAT GATTGTAAGA GTGTTTGAAA AGGTAACACA TCTCCTTTTC	420

1112

CTTAGCCACA CTTTTTAACC TTTTGCACAG AGGTTAGTTT TTGTTTCATCT CATAGTTAAT 480
 GACATGAAAT AGAGGTTGGC AAACTTTTTC TCCAAAGGGC CAGATGGTAA ATAGTTTGGG 540
 TCTTTTGGGC CACATGTGGT CTCTGTTGTG TATTGTTTC 578

(2) INFORMATION FOR SEQ ID NO: 686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686:

TACGCCTATT TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG TCAGGTGGCA 60
 CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT TTTCTAAATA CATTCAAATA 120
 TGTATCCGCT CATGCAATAA TGAATACGCT CAGGAGACAG CCGCTAACCC AAATTGCGCG 180
 CAAnGGGTAA TGAAGGTGAG GGATATATAT CTGCGTGTG AGTTTAGTCC AGAAAATCCT 240
 GCGCAGACAT CTGCCCTTTC TTTTCCTCAG AGTAACGTGC TGCAGTATTT TGTACAGGGT 300
 GGCAGTATGT AAGTATACGA CCGAGTGGAA CAGAACAAA AATAAAGTGT TATATCATCC 360
 ACCCTCTGGA CCGTCATACC TCGATAGAAG AAGCAGAACA GCGGGGGCAA CAGGTTATCA 420
 CCGCnTTGAA CCAGAGGnGG GGACATATCT GCCATGGTAT A 461

(2) INFORMATION FOR SEQ ID NO: 687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687:

CCCTGATAAG ATTTTAGACT CCTACTCTCC TTCGCACGAG AGTCCGGTCA GTCACCACCG 60
 TGCGCGTATA TTCGGGGGAG TATTTCTCAC CAATAACATG CTGCAGCACG ACTGCGCATC 120
 AGACGTGGGG CATAAGAAAG AGAATGCAGC GAACGTCAAT GGCACCGTGA GCGCCGGCAC 180
 GCGGGGCATT GCATCCGAAG ATGGTAnCGC CGGAAACCTC AAGCATGGAA AGCCGCGCGC 240
 AAAAGACGCA ATTCCACCCT GACGGGGAGG GCAAGTCAA CACGGGCGCC GCCCCAGCAG 300
 GAAGAAACCA CAGCGCCGCG TTTGCACGCT ATGCTCCTGC TACGAATGGA AGGCAGAATA 360

1113

TTGTGGGTAT TACGAGTGTG GGGTAGTGGT CAATCCGTTA GAGAAGGTGG AGATTCGGCT	420
GAAGCTGGGA GCAAnGCAAA GCTACAAGAG AACAGCAATG TAGTGATAnA GAAAAACGTG	480
ACGGAGCGTT TGCAATTCGT AAGGGCAT	508

(2) INFORMATION FOR SEQ ID NO: 688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688:

ACTTCAAGAA CTCTGTAGCA CCGCCTACAT ACCTCGCTCT GCTAATCCTG TTACCAAGTGG	60
CTGCTGCCAG TGGCGATAAG TCGTGTCTTA CCGGGTTGGA CTCAAGACGA TAGTTACCGG	120
ATAAGGCGCA CGGGTCGGGC TGAACGGGGG GTTCGTGCAC ACAGCCCAGC TTGGAGCGAA	180
CGACCTACAC CGAACTGAGA TACCTACAGC GTGAGTATGA GAAAGCGCCA CGCTTCCCGA	240
AGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAAGGTCCG AACAAGAGAG TTCGCGTAAC	300
GTTTCACATG GAAnAGCAGC GCTTCCCGAA GCCAACACAC GTTGCAAAAG GCGGCACACG	360
AATTTTCAAG CACTGGGGCA nCTGGnCAGA GGGCACGGAT CGCTAnCTGC TCTCCGATTC	420
AAGCCGGCGC AAAGTG	436

(2) INFORMATION FOR SEQ ID NO: 689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689:

TGCAGGTAAC ATCTCTAGGA CCTCACTATC ATTGCTTTAT ATCACTATTT TATTTAATAG	60
GCTTTTTTTT TGTTTTTGAC AGGCAGAGTG CACAGTGAGA GAGAGAGAGA GAGAGAGAGA	120
GAAAGGTCTT CCTTTGCCGT TGGTTCACCC TCCAATGGCC GCTGTGGCCG GCACACGGCA	180
CTGATCCGAA GCCAGGAGCC AGGTGCTTCT CCTGGTCTCC CATGGGGTGC AGGGCCCAAG	240
CACTTGGGCC ATCCTCCACT GCACTCCCGG GCCACAGCAG AGAGCTGGCC TGGAAGAGGG	300
GCAACTGGGA CAGGCTCCGG CGCCCCGACC GGGGCTAGAA CCCGGTGTGC TGGTGCCGCA	360

1114

GTGGAGGATT AGCCTAGTGA GCCACGGCGC CGGCCTTTCA TAGGCTTTTA ACCCAAGCCT	420
GGCACCCCAA GATTTCAGAA GCTCCAAGAG GACTTTGCTG TTTACATTAG CACAGGTTTT	480
ATTATAAAAn nGCTGATTG GGCCTCCTTC TCTAATTAAT AGTACTTTTA GnCACATTTT	540
TAAGATGTTT ATGAAGATGT TACTGCATTG CTGCATTAT GATTACnGTA AGACACCTCA	600
AAG	603

(2) INFORMATION FOR SEQ ID NO: 690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690:

ATAATTCTAA AATTTCTGTC ATTTTCAGGGT TGACACGAGG CTGGTGCCGT GGCTCAATAG	60
GCTAATCCTC CACCTAGCGG CGCCGGCACA CCGGGTTCTA GTCCCGGTCTG GGGCGCCGGA	120
TTCTGTCCCG GTTGCCCCTC TTCCAGGCCA GCTCTCTGCT GTGGCCAGGG AGTGCAGTGG	180
AGGATGGCCC AGGTGCTTGG GCCCTGCACC CCATGGGAGA CCAGGAGAAG CACCTGGCTC	240
CTGCCTTCGG ATnAGCGnGG TGCCTGACCT GCAGCGCGCC GGCTGCGGCA GCCATTGGAG	300
GGTGAACCAA TGGCAAAGGA AGACCTTTCT CTCTGTCTCT CTCTCTCACT GTCCACTCTG	360
CCTGTCAAAA AAAAAAAAAA AATACTGTGT CTTGGGGCTG GCATGTGGTG CTGAAAATCC	420
CATATGGGCG CTGGTTTCGAC TCCCAGCTGC TCCACTTCCA TCCAnCTCTC TTCTATGGCC	480
TCAGAAAGCA GCAGAAGATG GCCCAAGTCC TTGGGGCCCT GCAACCATGT G	531

(2) INFORMATION FOR SEQ ID NO: 691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691:

GAGCAAGGCA AGACTACAAG AGAACAGCAA TGTAAGTATA GAGAAGAACG TGACGGAGCG	60
TTGGCAATTC GTAGGGGCAT GTCGCTTGAT TTGGTAGAGA ACGGCATGCC CGTCTATTAC	120
TTGCGAGCCC GAGCCCAACT CCCAGCCGTA GCCCCAGCCA ATGACATCTT ATGGGACGCA	180

1115

GGCKTACATG CCCgTCCATT GGAACGCCTT cACCCAAGCC CGAGCCCTGC CCGGAGCCCC	240
AkTCCCAGCC ATCTACTTCC CGGTTGTAGT TACAATTCCA CGCTTTCTGG CGACTATGCC	300
CGAGCCGAG CCGCAGCCGG GGCTGGAGTC GACATCAACT TCCCGGTGTA TGGGGGTGTC	360
TTGCACGCAT CGCAGGCTAG TAATGTATTT CAGGGTGTCT TTCTCACC GA TACCACACCC	420
ATGCGGACGC ACGACATACC CCGCAGTCCC CTCGTGGGGC ATAAGAAAAA CGCAGCTCCC	480
GATGGCATAG GCGCCTCACG CGCGTGCTGC CCAGCGCGCG AGAACGAACC CTTTAAAAAG	540
GGTTCGACAA ACAGCCGTGG GGGGGGGGTA GAATGGAGTA GGTCTCGAC GAGACGCGTA	600
AGAGGATCGG CGTTGGAGCG GGGTATGAA	629

(2) INFORMATION FOR SEQ ID NO: 692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692:

GATACCCAAT AAATTCAGTG TCTGGATTTC CTCGGGAGAG TTTCCATTGG ATTCCTGTGG	60
CTGTATCATA CCTTCTTTAG TGTGTGTCCC ATTTTTTGTG GTTGTGCTG TTGTTGGTAA	120
TTGATATAT ATATTTTTTT TTTGACAGGC AGAGTGGACA GTGAGAGAGA GAGACAGAGA	180
GAAAGGTCTT CCTTTGCCGT TGGTTCACCC TCCAATGGCC GCCGCGGCCG GCACGCTGCG	240
GCCGGTGAC CGCGCTGATC CAAAGGCAGG AGCCAGGTGC TTCTCCTGGT CTCCCATGGG	300
GTGCAGGGCC CAAGCACCTG GGCCATCCTC CACTGTACTC CCGGGCCACA GCAGAGAGCT	360
GGCCTGGAAG AGGGGCAACC GGGACAGAAT CCGGCGCCCT GACTGGGACT AGAACCTGGT	420
GTGCCGGCGC CGTGCACTG GCCGGTAATT GGATATTGCA AATAATTGAT ATTTGGCAAC	480
TTTAGGAAGC AGATGCTCTT AATGAACAAG GTTGCTGTTG TTGGCTTCAA TGTTTAATGC	540
C	541

(2) INFORMATION FOR SEQ ID NO: 693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693:

AACGCCTGGT ATCTTTATAG TCCTGTCGGG TTTCGCCACC TCTGACTTGA GCGTCGATTT	60
TTGTGATGCT CGTCAGGGGG GCGGACTAAT GGAAAAACGC CAGCAACGCG GCCTTTTAC	120
GGTnCCTGGC CTTTTGCTGG CTTTTGCTC ACATGTTCTT TCCTGCGTTA TCCCCTGATT	180
CTGTGGATAA CCGTATTACC GCCTTTGAGT GAGCTGATAC CGCTCGCCGC AGCCGAACGA	240
CCGAGCGCAn GGTTCAGTGA GCGAGCCGCG CGTGTTCCTA ATAAGGTGGG GCTAGAGGAG	300
GATCCTTCTA ACTTCTTGCT TATGCACGCG ATGGGTCCTA ACGTGGCTGG TGTCATTGGG	360
ACCGCGATAC CGCAGGTGT TCATCTCGGC CTACGGAGGG TAGGGAGGAA GAGTAACCGC	420
GGGGTTTGC CGCTTAGGTA ACCTTTCCTC CGTGCGCGGG CAnAnCCTCT CAnGTGGGCT	480
AAGGGGnTTT TGCAGACGAA GCGGG	505

(2) INFORMATION FOR SEQ ID NO: 694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694:

AAGAGATTTT TTTTGTACAG GCAGAGTGGA CAGTGAGAGA GAGAGAGAGA GACACAGAGA	60
AAGGTCTTCC TTTTGCCGTT GGTTCACCTT CCAATGGCCG CTGCGGCCGG CGCACTGCAG	120
CCAGCGCATC GCCTGAATCC AAAGCCAGGA GCCAGGTGCT TTTCTTGGTC TCCCATGGGG	180
TGCAGGGCCC AAGCACTTGG GCCATCTCC ACTGCACTCC CTGGCCACAG CAGAGAGCTG	240
GCCTGGAAGA GGGGCAACCG GGACAGAATC CAGCAnCCCCA ACTGGGACTA GAACCTGGTG	300
TGCCAnCGCC GCAAGGGGAG GGATTAGCCT ATTGAGCCAA AnCGCTTGGC CAGCAAAGAG	360
ATTTGGATAT TTCATTTCCTA TTACAGCCAA GGTTCGTTCA GGTCAACTAG GAGCCAGGAA	420
TCTTATCCAG GTCTCCCCAC GTGGGTGACA GGGACCCAAA TATTCAGCTT TCATCGTTTG	480
CTCTAnGCTA ATGnATTAAC ATGAAAGCTA AATTGGATGT TGTAA	526

(2) INFORMATION FOR SEQ ID NO: 695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695:

GGTGCAGCGG CTCAGTAGGC TAATCCTCTA CCTGCGGCG CCGGCACATC GGGTCTAGT	60
CCCGGTCAGG GCGCCGGATT CTGTCCCGGT TGCCCTCTT CCAGGCCAGC TCTCTGCTGT	120
GGCCCGGAAG TGAAGTGGAG GATGGCCCAA GAACTTGGGC CCTGCACCCC ATGAGAAGAC	180
CAGGAGAAGC ACCTGGCTCC TGCCATCGGA TCAGCGCGGT GCACCGGCCG CCGCGCGCCA	240
GCCGTGGCGG CCATTGGAGA GTGAACCAAC TGAAAAGGA AGACCTTTCT CTCTGTCTCT	300
CTCTCTCACT GTCCACACTG CCTGTCCAAA AAAAAAAAAA AAAGAnnAGA AGAAAAAAAA	360
AAAACACTTT GATGTAAATA TGTCTTTAA AAAAAAGTAT GCTCAATTTT TATTATATTA	420
TTAAAnAGTAT TCTAAAAACn ATATAAAGGG GT	452

(2) INFORMATION FOR SEQ ID NO: 696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696:

CTGCTGCCAG TGGCGATAAG TCGTGTCTTA CCGGGTTGGA CTCAAGACGA TAGTnACCGG	60
ATAnCnCGCA CGGnTCGGGC TGAACGGGGG GTTCGTGCAC ACAGCCCAGC TTGGAGCGAA	120
CGACCTACAC CGAACTGAGA TACCTACAGC GTGAGCTATG AGAAAGCGCC ACGCTTCCCC	180
AAGAGAAAGG CGGACAGGTA TCCGGTAAGC GGCAGGGTCG GAACAGGAGA GCGCACGGGA	240
AATAAAGGCC ATGCGCGTGA AGTGCGTTTC TCCAAGCGAG CTTATCAGTG CGCTCAGCGG	300
GGGTAATCAG CAGAAAGTCA TTATTGAAA TGGCTCGAAC GCGATCCCGA CGTCCTCTTG	360
CTTGATGAGC CGACCAGGGG GATCGACGTG GGTGCGAAAT ATGAAATTTA TCAGCTCATC	420
ATTCGTATGG CGCGTGAGGG AAAGACAATC ATGTGGTTTC TAGTGAAATG CCTGAAATTC	480
TT	482

(2) INFORMATION FOR SEQ ID NO: 697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697:

GTTGGTTTAC	CCTCCAGTGG	CCGCCGCGGC	CAGTGCCTG	CGGCCAGCGC	ACCACGCTGA	60
TCCGATGGCA	AGAGCCAGGT	ACTTCTCTG	GTCTCCCATG	AGGTGCAGGG	CCCAAGCACT	120
TGGGCCATCC	TCCACTGCAC	TCCCGGGCCA	CAGCAGAGAG	CTGGCCTGGA	AGAGGGGCAA	180
CCGGACAGA	ATCCGGCTCC	CCGACCGGA	CTAGAACCCG	GTGTGCCGGC	GCGGCAAGGT	240
GGAGGATTAG	CCTAGTGAGC	CGTGGCGCCG	GCCGCGATTG	TGTTTAAACA	TGCGTGCACA	300
TCTGCCTGAA	GACAGTTCAA	TTCTGATCTG	CCTTGAGTCG	CTGAGAATCT	TTCTTCCCAG	360
TCTGTTATTT	ATCATCTGTC	ATAAGCATGA	CCTGAAATGC	TGATTGGAAT	CATCATCTG	420
ATAAGATCCT	AACATCTCCT	TCTCTGAAAT	TTTTCTATAA	TTTCTCTGGA	ATAAATTGTG	480
AATATACAAG	GCTTACTAAT	AACATTTCTT	TATCAGATAT	TAATAACATT	GTTCGTCTGC	540
TTTTGGCTCC	CTTTGTCTCT	CTATTGAGGG	CCTTATTGCA			580

(2) INFORMATION FOR SEQ ID NO: 698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698:

CGCTGCGGCT	CACTTGGCTA	GTCTCTGCC	TGCGGCGCCT	GCACCCTGGG	TTCTAGTCCC	60
GGTCGGGGCG	CTGGATTCTG	TCCCGTTGCG	CCCTCTTCCA	GTCCAGCTCT	CTGCTGTGGC	120
CTGGGAAGGC	AGTGGAGGAT	GGCCCAAGTG	CTTGGGCCCT	GCACCTGCAT	GGGAGACCAC	180
GAGGAAGCAC	CTGGCTCCTG	CCTTCGAATC	GGCGCACGTG	CTGGCCGCAG	TGCGCCACCG	240
TAGCAGCCAT	TTGGGGAGTG	AACCAATGAA	AGGAAGACCT	TTCTCTCTGT	CTAACTCTGC	300
CTGTCAAAAA	AAAAAAAAAA	AAAAAAAAAA	GGATGATAGA	CTATGAGCTG	TGACTATTTT	360
AAAATTTATT	GTATATGAGT	GAAATAGACA	TCTTTTCATT	TATTACTGCT	TATGGCCTTG	420
CCTATATTCC	TGCGGAACTA	TGGTGTTTTT	ACTTGTGAA	CTCTTTATTT	AGTGGAGCAC	480
TAAAGATTTG	ACTATTTGTA	ATGnATGTTA	AAAATATGTT	ATCTTGGGGC	CGGAGCTGTG	540
GCACAGCAGA	TTAATGCCTT	GGCCTGAAG				569

(2) INFORMATION FOR SEQ ID NO: 699:

1119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699:

TGTAAATTAT GTGTTGAGAG GGTACCTTT TTTTTTTTTC AAAATAAATT GTTGCCACTA	60
GGAAAAGAGG GCAATGTATT TTGTTAAATT TGGTTGCTAA GAAATGATGT GTTAGTCACG	120
TGAATTCTCT CAAACATCAG ATACTTTTCT GCTTCAAGGC CTTTATTTT GTAGGTACAT	180
TGCCTAAAAA AATCTTTTTT TTTTTTTTTT TTTTTTTTTT TTGACAGGCA GAGTGGACAG	240
TGAGAGAGAG AGACAGAGAG AGAAAGGTCT TCCTTTGCCG TTGGTTCACC CTCCAATGGC	300
CGCCGCTGCA GCCGGCGCAC CGTGCTGATC CGATGGCAGG AGCCAGGAGC CAGGTGCTTT	360
TCCTGGTCTC CCATGGGGTG CAGGGCCCAA GCACCTGGGC CATCCTCCAC TGCACCTCCT	420
G	421

(2) INFORMATION FOR SEQ ID NO: 700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700:

CCCTTGGGTA AATTCCCAGG AGTGAGAGGC CTGGGTCATA TGATAGGTCT ATATTAGATT	60
TATTTTAAAT ATTTATTTAT TTGAAAGAGT AACACAGAGA GAGGAGAGGC AGAGAAAGAG	120
GGATCTTCCA TGCAATGGTT CACTCCTGAG TTGGCCGCAA CAGCCGGAGC TGTGCCAATC	180
TGAAGCCAGG AGCCAGGAGC TTCCTCTGGG TCTCTGACGT GGATGCAGGG GCCCAGGGAC	240
TTGGGCCATC TTCTACTGCT TTCCCAGGCC ATACTAGAGA GCTGGATAGG AAGTGGAGGA	300
GCCAGGACTA GAACCAGCGC CCATAAGGGA TGCTGGCGCT TCAGGCCAGG GCATTAAACC	360
ACTGnCGCTA CAGCGCCGGC CCTGGTCTAT ATTAGATTTT GAGATATCTC TATACTGTTG	420
TCCACAGTGG GCTTTACCAG TTTACATTCC CACCAGTAGT GGATTAGGGT ACCTTTTCCC	480
CCACATCCTC GCCAGCATTT GTTGTGTTGAT TTCTGTATGA AAGTCATTCT AACTGGGGTG	540
AGGTGAAACC TCATTGTGGT TTTTGATTG CATTTCCCTG GATTGCTAGT GATCCTGAGC	600

1120

ATTTTAAAT GTATCTGTAG CCATTGGAT TTCCTCTTC GAGAAATGTC TTTTAAAGTC 660
CTTTGCCCAT TTCTTGACTG GGGCTGTTG TTTTGTGAT G 701

(2) INFORMATION FOR SEQ ID NO: 701:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701:

CCACCGCTA CCAGnGTGGT ATCTGTTTGC CGGATCAAGA GCTACCAACT CTTTTCCGA 60
AGTAACTGGC TTCAGCAGAG CGCAGATACC AAATACTGTT CTTCTAGTGT AGCTTGTGTA 120
TTAAGGCGAn CGATGCAGAn GAGGTAAGTG GGGATCCCGA TGACACGGAG ATGGAGTATT 180
TACCTCCCCG nTATGCGCCG GAGACGCCGC TGGnGGGACT CGATGTGGCG TTCCGTGCGG 240
ACAATGG 247

(2) INFORMATION FOR SEQ ID NO: 702:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702:

AAGTCACTTG CTGCTGCTTT CTTAATAGCA TTAAGAGGGA GATGGATCAG AATTGGAGCA 60
ACTGGGACTC CAACCAACAC CCATATGGGA TGCTGGTGTT GCAGGCAGCA GCCTTAACCA 120
TTATGTCACA TCACCATCCC CAAAGGGAAC TTTATAGCAG TAAATGCTAT AGAAAACAAA 180
ACCCGGGGCC AGCACTGTGG CATAGCAGGT AAAGCCGCCG CCTGCAGTGC CAGCATCCCA 240
TATGGGCACC AGTTCGAGTG CCAGCCACTC CACTTCAATC CAGCTCTCTG CTGTGGCCTG 300
GGAAAGCAGT AGAAGATGGT CCAAGTGCTT GGGGCCCTGC ACCCAGTGG GAGACACAGA 360
AGAAGCTCCT GGCTCCTGGC TCGGATCTG TGTAGCTCCA GGTATTGTGG TCAACTGGGG 420
AGTGAACCAG CGGATGAAAG ACCTCTCTCT CTCTCTCTCT CTGCCTCTTC TTCTCTCTCT 480
GTGTAACCTG ACTTTCAAAT AAATAAAAT AAATCTTATA AAAnAnAAAA ACACAAAGAT 540
CTCAAATCAG CAACCTTAGT TTTGTACAAT AAA 573

1121

(2) INFORMATION FOR SEQ ID NO: 703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703:

CCTCGTGCGC TCTCCTGTTT CGACCCTGCC GCTTACCGGA TACCTGTCCG CCTTTCTCCC	60
TTCCGGGAAGC GTGGCGCTTT CTCATAGCTC ACGCTGTAGG TnCGGCTCCC TnCCCTTTGC	120
TGATGAAACA GAAAAGCTTG CCTGGCTCGC GCGCCAAGGT TTCGTGACGG TACATTGCGA	180
TCGCTGCGCT AACGCACAGG AAGTTGTTGC ACTCCGATCT GAGATTATGC GCACGCGCGA	240
GCTGTTGnCT TACAnGATCG ATGGCCTGGT AGTAAAGAGT ACCGATCTTG GACTTCCAGG	300
ACGTA	305

(2) INFORMATION FOR SEQ ID NO: 704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704:

AnATCGACGC GGAActGGCC GCCACGGCGG CGCACCACGC TGATCCGAAA CCAGGAGCCA	60
GGTGCTTCCT CCTGGTCTCC CATGCGGGTG CAGGGCCCAA GCACTTGGGC CATCCTCCAC	120
TGCACTCCCG GGCCACAGCA GAGAGCTGGA CTGGAAGAGG AGCAGCCAGG ACAGAATCCG	180
GCGCCCCAAC CGGGACTAGA ACCCAGAGTG CCGGCGCCAC AGGCAGAGGA TTAGCCTAGT	240
GAACACGGCG CCGGTCCGGG GCTTTATTTT GCTTGAGGAC CTCTATTGGT CATTATTGGT	300
CACTCCGTCT CCTCCACTGC CCTGTCTGAG CTTTGTCTGC TCCTGTCTCT TTTAGGCCTA	360
GAGGTGACTT TTCACCCTGG GGTGCCTCTG ACACCCTTTC CTGCTnCTCC TTCAACCCCA	420
AGCACAGCTT TGCAAATCCA TCTTCTATGA TGTGGCCAGA TnGGGTGTGG TATCAGCTCT	480
TGCCGGGGCT	490

(2) INFORMATION FOR SEQ ID NO: 705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs

1122

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705:

GCTCTGGCCC AGAAGTACTG TGGAGGATGG CCCAAGTGCT TGGGCCCTGC ACCCACATGG	60
GAGACCAGGA GAAGCACCTG GCTCCTGGTT TCGGATCAGC ATGGTGTGCC AGCCACAGCG	120
CGCCACCACA GCCACCAGTG GAGGGTGAAC CAACGGTAAA GGAAGACCTT CCTCTCCGTC	180
TCTGTCTCTC TCACTGTCCA CTCTGCCTGT AAAAAAAAAA AGAAGTAAAC ATGAAACATG	240
TCACCACCAA ATTCACTAAC ATTCAAGGTAG GATCATTATC CAACCAACAA AATGACAGGT	300
CTTAATTTTT ATTTCTCAGT ACTAACCTTG AATGTAAATG GATTAAATTC ACCAACCAAA	360
AGACTTAGAG TGGCTGAATG GATTAAGAAC CATGACCCCA TTATATGCTG CCTACAAGAC	420
ACTCATTCCA CAAACAAAAG TACACACAGA CTTAAATTGA AGGGTTGGGA AAACATATAC	480
CAAGCAAATG GAAACCCAAA ATGAGCAGGC ATAGCTATCA CAATATTCAA TGAAACAGAC	540
TATAAATCAA AAGCTATTAA AAAGATTAAG AAGGnCATTA TATTTTGATA AAAG	594

(2) INFORMATION FOR SEQ ID NO: 706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706:

ATATAAGTGA GATCATGTAG TACTTGTCTT TCTGGACTGG TTTATTTGTA ATTCATGAT	60
CTCCAAGTCC ATCCATGTCA TTGCAAATGA CAGGAATTCA TTCTTCATAA GGCTGAATAG	120
TATTCCATTG TGTTATGTAC CACGATTCCT TTATCCATTC AGGGTTTATG GACACCTAGG	180
TTGATTCCAC ATCTTGGCTA TTGTGAATAG TGCTGCAGCA AACGTGCGGC TTTAGATATC	240
TCTTCAACAT ACTTATTTAA TTTCCTTTGG ATATTTTTTT TTTTGAGCGG AGTTAGACAG	300
TGAGAGAGAG AGACAGAGAG AGACAGAGAG AAAGGTCTTC CTTTGTGTTGG CTCACCCCA	360
AATGGTTGCT ACGGGCTGGT GCGCTGCGCC GGATCTGAAG CCAGGAGCCA GGTGCTTCCT	420
CCTGGTCTCC AATGTGGGTG CAGGGCCCAA GCACTTGGGC CATCCTCTAC TGCCTTCCTG	480
GGCCATATCA GAGAGCTGGA TTGGAAGAGG AGCAACCAGG ACAGAATCCG GCA	533

1123

(2) INFORMATION FOR SEQ ID NO: 707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707:

```
GnGAGGCAnA GAGAGAGAGG TCTTCCATCT GCTGGTTCAC TCCCCAATTG GCTCCAATGG      60
CTGGAAGTGA GCCAATCGGA AGCCAGGAGC CAGGAGCTTC TTCCGTGTCT CTGACACAGG      120
TACAGGGGCT CAAGAACTTG GTCCATCTTC TACTGCTTTC CCAGGCCATA GCAGAGTTGG      180
ATCAGAAATG AGGCAGCCAG GACTTGAACC AGCACCCACA TGGGATGCCA GCACTGCAGG      240
CAGCAGCTTT ACCCATTACA CCACAGTGCC AGCCCTTCAA CTATTTTAA TAGATCACTT      300
TTTTAAAAAT AGAATTTATC AGG                                         323
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(2) INFORMATION FOR SEQ ID NO: 708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708:

```
ATGATAAAAT ATTTGTAATG ATCCTTAAAA TCTTCTTAGA ACAATTATGT ATGTATGTAT      60
GTAACAATTC AGGTTTATTA TTTATAAGTT TGTTCCTTTG AAAGAGTAGG GGGCCAGCAT      120
TGGAGCACAG TAGGTTAAGC CACTGCATGT GGTGCTGGCA TCCCATATGA GCAGTTGTTT      180
GAATCCACTT CCAATCCAGC TCCCTGCTAA TGTGCCTAGG AAAGCAATGG AAGATGGTTC      240
AACTGCTTGG GTCCCTGCTA CCCTGTCTCT ATATGGGAAA CCTAGATGGA GTTCTAGACT      300
CCTGGCTTCT GTTTGGCCCC ATCCTGGCTG TTGCAGCTAT TTGGGGAGTG AACCAGCAGA      360
AAAGTTGTAA GTGATAGAAT TAGGACTTTA GTTATGGGAG GATAAAGCAA ATACATTTTG      420
GTCTACAAGA ATCGCAGATT TGGAGAAAGT AAGAGTAATA AGGAAAAGTT TAAAAACTGT      480
AGGTGAGGCC GGCACCGCGG CTAAGTAGGC TAATCCTCCA CCTAGCGGCG CCGGCACACC      540
GGGTTCTAGT CCTGGTCGGG GCGCCAGATT CTGTCCCGGT TGCCCTCTT CCAGGCCAGC      600
TCTCTGCTGT GGCCAGGGGA GTGCAGTGGA                                         630
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1124

(2) INFORMATION FOR SEQ ID NO: 709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709:

```

CCAAGTATAA GTCATGAAA GCATTTGTTT ATTTTATCTT TATTGATTTG CCTTTCATAC      60
TTAGACCTAT AATGTATCTG GGCTTGATTT TTGCATATAG TGTGAAATAG AATTCTACAT      120
ATCTGGGGCT GTTGCTGTGG CGTAGTGGGT AAAGCCACCG CCTGCAGTGC TAGTATCCCA      180
TATGGGCGCG GGTTCAGTC CTGGCTGCTC CTCTTATGAT CCAGCTCTCT GCTATGGCCT      240
GGGAAGGCAG TAGAAGATGG CCCAAGTCTT TGGGCCCCCTG CACCCACATG GGAGACCTGG      300
AAGAAGCTCC TGGCTTTGGA TTGGCTCAGC TCTGGCCGTT GCAGTTAATT GGGGAGTGAA      360
CCAGCAGATG GAAGACCTCT CTCTCTCTCT GTGTAACCTT GACTTTCAAA TAAATAAATC      420
TAAAAAGTAC ATATCCAGTT GGATGAAACA CTTTATTGAA AAGACAATTG TCTGTCCAC      480
TGCTATGTAG TATCTTATAA TTAGAACAAT GACCATTAA TGACTGATCT GTTTTCAAAT      540
TCTGnATTTT TCTGCTCCTG TCCTTTTAA nTTTT      575

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(2) INFORMATION FOR SEQ ID NO: 710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710:

```

AGGAAGACCT TTCTCTCTGT CTCTCTCACT GTCCACTCTG CCTGTCAAAA AAAAAAAAAA      60
AGGTATTTCT TCTGTnGGTT CACCCCCCAA ATGGCTGCTA TGGCCGGCGC ACTTGCCGAT      120
CTGAAGCCAG GAGCCAGGTA CTTCTCCTGG TCTCCnATGC AGGTGCAGGG CCCAAGGACT      180
TGGGCCATCC TCCACTGCAC TCCTGGGCCA CAGCAGAGAG CTGGCCTGGA AGAGGGGCAA      240
CCGGGACAGA ATCCAGCACC CGGACCAGGA CTAGAACCAG GGATGCTGGC ACCGCAGnGA      300
GnGATTAGCC TAGTGAGCCG CGGCGCTGGC CACAACCCCT GAATTCTTGA CCTGTGGAAA      360
CAATCTAGTC AATTTGTATT GCTGTTTCAA GTCAGTGCCT TATGGGTCAT TTGTTTGTCT      420

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1125

GCAGTTGACA ATTTAGTGTA TGTGGTAGGG TGGAAGAGCA TAGAACATGC TAGCTCCAGA	480
TAAAATTCCC GAGTCTAAGG TCGATAGCAG GGATACAGAG AAAGGAATCA GATTCTCTTT	540
CACTAGCAGG TCCAGACAAG CATAACAGCAG GCAGGTCCAA CAAACAGGTG CTAGAGAGGG	600
GATGCCTCCT CCCCACTTCT CTTGGGTTTC CAGAGAAACC GATGGATTAG CCCCTGCTTG	660
TCTAAAAGAG GGGGGAAAAT AGCTTGAGAA T	691

(2) INFORMATION FOR SEQ ID NO: 711:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 667 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711:

GAGAGAGAGA GAGAGAGAAA GGTCTTCCTT CCGTTGGCTC ACCCCCCAAA TGGCCGCAAT	60
GGTCGGAGCT ATGCCAGTCC GAAGCCTGGA GCCAGGTGCT TCCTCCTGGT CTCCCAAGCG	120
GGTGCAGGAG CCCAAGTACC TAGGCCATCC TCCACTGCCC TCCTGGTCCA CAGCAGAGAG	180
CTGGACTGGA AGAGGAGCAA CTGGGACTAG AACCCAGCGC CCATATGGGA TGCTGGCGCC	240
GCAGGAGAGG ATTAACCAAG TGAGCCATGG CCCCCAGTAT AATGTTTTAA GTTGTATTTT	300
TCCTGAAACA AAGAGTTGAG TGTAATGGA TTATTTGGAA AGTGATCCAG AATCACTGTA	360
TGGGGAAGTA GGAAAGAGAG TGGGAAACGA AGGAAGTCCA AACAGGGTAC AGGATTAATT	420
AATTAAGCTA TTAAGTGGG TAACGAAGGC TCAAGCCTAC TCAGGGAGAC TACATGAAAT	480
TTGCCCCACA GGTGCCTTAC CCAAGGAAGT TGGGGTATTT ACAAATTCGT ATCCATCACT	540
GGATGATGGG CTTGCTTGAC TGAGTGTTG TTAATTCCT ACATAAGTGT GGACCTGCCT	600
CTCTCCTCCC CCTGAGAAAG CCTGAGGGGC AGAGCCACAC TGCTTACAGT AAAGAGATCA	660
CATGTTT	667

(2) INFORMATION FOR SEQ ID NO: 712:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712:

1126

nAACCTTCCTT TCTTTCTTTC TTTCTTTCTT TCTTTCTTTC TTTCTTTCTT TCTTTCTTTC	60
TTTCTTTCTT TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC TCTTTCTCTT TCTCTTTCTn	120
nnTTTCTCTC TTTCTCTCTT TCTTTCAAGA TTTATTCATT TATTATTTGA AAGGCAGAAT	180
TACAGACAGG CAAGGnAGAC AGAGAGAGGC TGGTCCTCCA TGGGACGGTT CACTCCCCAA	240
ATGGGCAAAT CGACTGGAGC TGGACGGATC CGAAGCCAGG AGCCAGGAGC TTCTTCCTAG	300
TCTCCCATGT GGGTGCAGGG GCCCAAnGAC TTGGGCCATC TTCTACTGCT nTCCCAGG	358

(2) INFORMATION FOR SEQ ID NO: 713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713:

TGATTTGAAA CAAATGTCT AAATCCTTCT AGAAAGTGTG TATTTAATAA ATACGTAAAT	60
ACAAAACCTT GACAGCTTCA TTCCAGAAA ACATCTCCTA TGCCCTGGTGA ACACAGACCC	120
CGGGGCCTCA GGCCAGnnGA CCTGTCCAGC TCCTTGTTGT TTCTGATCAT GAAACAGGGT	180
TAAGATGTTG CACAGTCAGA CTCACCAGTC TCACTTCCTG GCCTTTGGGA ATTATGCACT	240
GGAAGGCTGT CACATCTTCA TTTTTTAAAG GAATTCATTT TTTTCAACCT AAATATCTTT	300
TATAAGAAAT AAGGCTGAGG CCGGCGnCGC GGCTCACTAG GCTAATCCTC CGCCTAnTGG	360
CGCCGGCACA CTGGGTTCTA GTCCCGGTCA GGGCGCCGGA TTCTGTCCCA TTGCCCCTCT	420
TCCAGGCCAG CTCTCTGCTG TGTCAGGAG TGCACTGCAG GATGGCCCAA G	471

(2) INFORMATION FOR SEQ ID NO: 714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714:

ATTTTTTCTT TTTTAAAAA CCTTTTTTGG GGCCAGCACT GTAGCGTATG GnGTAAAGCT	60
GCCGCCTACA GTGTCAGCAT ACCACATGGG CGCCAGTTTG AGTCCCGGCT GCTCTACTTC	120
CAATATAGCT CCCTGCTATG ACCTGGGGAA GCAGTGGAAG ATGGCCCAAG TGCTTGGGCC	180

1127

CCTGTACCCA CATGGGAGAC CCGGAAGAAG CTCCTGGCTC CTGGCTTTGG ATCAGTGCAA	240
CTCCAGCCGT TGCGGCCATC TGGGGAGTGA ACCAGTGAAT GGAGGACCTC TCTCTCTCTC	300
TCTCTCTTTC TCTCTGCCTC TCCTCTCTCT CTCAATCTCT GCCTCTCTGT AACTCTGCCT	360
TTCAAATAAA TACATAATTT TTTTTTAAAA AACACCTCTT TCCTATTTTA TGGCATAACA	420
AGATGGTACC TTATACCTGT ACCTGCCCTG CCTGGGCTTG GGAATCACTC ACTTCTCTGA	480
GGGGTCCTGA TTCTGGTTTA ACAGACCAAG ATGTAAGTGC CAGATGATGT TTTTCTGAT	540
GAGTAAATC AATGGTAAAG CCATGTCTGT AAAGGTTGG TCTTTTGATT ATTTTGTCTA	600
AAGTATTACC TTTTTTTTTT TGACAGGCAG AGTGGACAGT GAGAGAGAGA C	651

(2) INFORMATION FOR SEQ ID NO: 715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715:

TCACATTGGG GGCCCATGCT GTGGCTTAGT GGGTTAAGCA GCCGCTTGCA GTGCCAGCAT	60
CCCATATAGA CACAGGTTCAG AGTCCTGGCT GCTCCACTTC TGATCCAGCT CTCTGCTATG	120
GCCTGGGAAA GCAGTAGAAG ATGGCCAAAT GCTTGGGCTC CTGCACCCAT GTGGGAGACC	180
TGGAAGAAGC TCCTGGCTCC TGGCTCCTGG CTTCCGATCA GCACAGCTCT GGTCGTTCTG	240
GTCATTTGGG GACATCTATC ATTAATTCAG TAAACACATA ATCCAATGGA ATTTTAAGCT	300
CATGATATGT GTCCTACTAC CCATCCATTT TTATTTTCAA GACCTCTTTT TCTCTCTCTG	360
CCTCTCCTTC TCTCTGTGTA ACTCTTCTT TTTTTTTAAG ATTTATnTnC TTTATTTGAA	420
AGAGTTACAG AGCAAAGTAG AGCCAAAGGA GGAGAGAGAG AGAAAGAGAG AGAGAGAGAG	480
AGAGAGAGAG AGAGAGAGGT GTTTTCCATC TGCTGGTTTA CTCCCCTAAT GAnCAGAATG	540
GCCAGAGCTG TGCTGATCCA AAACCAGGAG CCAGGAGCTT CT	582

(2) INFORMATION FOR SEQ ID NO: 716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716:

AAGATCTTTC TCTTTCCCCA TCTCCCTCTG TAACTCTGCC TTTCAAACAA AATAAATAAT	60
TTGTAAAAAG GCTAGTTTAT TTGAAAGGCA GAGTTACAGT GAGAGACAGG GAGAGAGAGA	120
GCTTTCTCGT CCGCTGGTTC ACTCCCCAAA TGGCCACAAT GGCCGGAAGT GAGCCAGTCT	180
GAAGCCAGGA GCCAGGAGCT TCTTCTGGGT CTCCCATGTG GGTGCAGGGG TGCAAGCACT	240
CGGGCCGTCT TCCACTGCTT TCCCAAGCAC ATTAGCCGGG AGCTGGACGG GAAGTGGAGC	300
AGCCGGGATT CGAACCAGTG CCCATATG	328

(2) INFORMATION FOR SEQ ID NO: 717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717:

AGGAGAGGAC AACTTCTCTC CCGGGTAGGG GCTGAGTCTG ATTCCTTTTG GGGTCCGTCC	60
CAGAGCAGTG TGGTTTGGTG CTGAGTAGGG GAGGGAAGAA TGGAGCCTGT GAAAGCCCCT	120
GTGAGAGGGA CAGGAGAGCC CGGCCCTGAG CCCCAGAGCC CAAGCGCGGA nGnGCCCAGG	180
CTCTGGAGTC CTGGGTGCTG GGTCTGGGTG TGCTATGATC TACAGAACCC CTGAGGATCC	240
TGACATGAGG GTCCATCTCT AGGCCCCAGA AAGTGGGTCA TGGGAATGGT GAGCTTAACG	300
ACTCGGGGCC CAGCAAGGCC ATGAGAGAGG GGGATGGGGG TAGGGTCCAG CTCCACTGTT	360
CCTTTTTTTTG TTTGTTTGTT TGTTTTGACA GGACAGAGAG AGACAGAGAG AAAGGTCTCC	420
TTACCATGGT TCACCCCCCA ATGGCCGCTG CGGCCAGCGC ACCGCGCTGA TnCCGAAGCC	480
AGGAGCCAGG AGCTTCTCCT GGTCTCCCAT GTGGGTGCAA GACCCAAGGA CTTGGGCCAT	540
C	541

(2) INFORMATION FOR SEQ ID NO: 718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718:

1129

GAGGTAAGTC TCATAATCCT ACACTTTTTG AAGTGAGATA ATACCTACTC CAGACAGTTA	60
ATGTGGATAT TAAATATGAT GTAACATAAC AGTGCCCAGC ACATAGTAGA TGTTTAAAT	120
ATGGAAGTTT TGGGGCTGGC ACTGTAGCTT AGCAGGCAAA GCTGCTGCCT TCAGTGCTGG	180
CATCCCATAT GGGAACTGGT TCGAGACCCA GCTGCTCCAC TTCTGATCCA GTTCTCTGCT	240
ATGGCCTGGG AAGCCAGGGT AAGAGGGCCC AAGTCCTTGG GCCTCTGCAC CCACATAGGA	300
GTCCTGGAAG AAGCTCCTGT CTCCTGGCTT CAGATCAGCA CAGCTCTGGC AATTGTGGCC	360
AAATGGGAGA ATGAACCAGC AGGTGGAAGA CCTTCTCTC CCTCTGTCTC TCCTCTCTCT	420
GTGTAATTCT GACCTCCAAA TAAATAAATA AATCTTTAAA AAATGCAAAG TTTCTCTCCT	480
CTCCACTACA CTCCAACCTT TTCCCTCACT TAATAATAA GACTCAGCTT GACCCACAG	540
GnACTCATCT TACATAGAAG AGCTAATACA TATGTCTAAA GCTGAAAAGT GAAGAAATGT	600
ATAGCAGACC TCTGCTCTCT	620

(2) INFORMATION FOR SEQ ID NO: 719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719:

GGGCCCCAAGC ACTTGGGCCA TCCTCCACTG CACTCCCCGGG CCACAGCAGA GAGCTGGACA	60
GGAAGAGGGG CAACCAGGAC AGAATCTGGC GCCCTGACCG GGACTIONAAC CCGGTGAGCC	120
AGCGCCGCAA GGAGAGGATT AGCCTGTAA GCTGTGGCGC CAACCTGTAT ACAAATTAA	180
AGTATGATTT TGTTTGGTTG GTTTTTTGAG GTATAATTTA AAAAAAAAAA GCTGTCTTTT	240
CCTTTTCTTG CTTTGTTTTC CGAAAAGCTA TCACGAGAGA AAACAACCTT TGTTTTTTAA	300
AGTTTAAAAA ACTTGCTTTG ACAAAGCTA ATAAATTATT TTTATTTTAA AATCAAATTA	360
ATATACTTTG GGGCGGTGCT GTGTACAGCA GGTGAAGCCA CnGCTGTGGT GCGGCGTCCC	420
ATATGGGCAC CAGACGCCCA TCAGCCCCAA CGCCACAAGC ACTACCGnAC CCAACAGGCA	480
CCTGCCACCC CACGCAGACG CATCAAATGG GCTCCTCCTG CCTCGCCGTT AG	532

(2) INFORMATION FOR SEQ ID NO: 720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

1130

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720:

AACGGGnCTG TGTGTAGGAT GTTAAGCTTC TGCCTGTGGT GACGGCATCT CATATGGATG	60
CCGATTCAAG ATCCAGATGC TCCACCCAAT CTAGCTCCCT GCTAATGGCC TGGGAGAGCA	120
GTGGAAGATG GCCAGAGTAT TTGGGCCCCT GCACCCACAT GGTAGAGCCA CAAGAAGCTC	180
CTGGCTCCTG GTTTTGGATG ATCCCAGCTC TGGTCATTGC AGCCATTTGG GGAGTGAACC	240
AGTGGACGGG AGATCTCTCT TTCTGTCTTT CCCTCTGTCT GTAACCTCTGC CTTTCAAATA	300
AATAAATAAT TTTTAAAAAT AAATCTTTCT TTAACAAAAA GGGAAAACAT GGGGCTGGTT	360
CTCTGATGTA GTGGGCAAAG CTGCCACCTG TGGTGCCAGC ATCCCATATG GCGCCAGTT	420
CCTGTTCTGG CTGCTCCACT TCCGATCTAG CTCTCTGTTG TGCCCTGGGA AAACAGTGGA	480
AAATGGCCCA ATCCTTTGGG CCCCTGCACC CACGTGGGAG ACCCGGAGGA AGCTCCTGGC	540
TCCTGGCCTC AGATCAGCCC AGCTCCGGCC GTTGTGGCCA CTTGGGGAGT GAGACAAAAG	600
AT	602

(2) INFORMATION FOR SEQ ID NO: 721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721:

AGTACAAGGG GGGCTTCAAC GAGTTCATGG AAAAATAGAC TCAAAAATGC TTAATTTTGT	60
AAATCCACGC ATAGTTACTT CTTGAAGACC CTGTCATGTA CTAGCACTCT GCCTCCTCTG	120
GCCTATTACG TTAAAAACAA CAACAACAAC AACAACAACA ACAACAACAG TTCACCTTTT	180
GCCTAGTAGC TCAGGTATCA CTTCTCTCTG GAAGACCACC AAGAATACAA TCAGAGAAGC	240
ATGAAACACA TAAGGAAACG GTAACCTGTG ATACACTCAC ACCAAGAAGT ACAACACAAC	300
CATTAAATAT CATATTTATT TTATTGGCAT AGGAAGAAAG TTGGCATTTA AAATATGTAT	360
ACGGGGGCCA GCACTGTGGT GTACTGGGTA AGCCACTACC TGCAGTGCCA GCATCCATTA	420
TGGGTGCCAG TTCAGGTCCT GGCTGCTCCA CTTCCAATCC AGCTCTTTGC TATGTCCTGG	480
GAAAGCAGCA GAAGATGGCC CAAGTCCTCG AGCCCTGCA CCCACGTGGG AGACCCGGAA	540

1131

GAAGCTCCTA GCTTTGGATT GGTGCAGCTC TGGCCATTGC AGCCATCTGG GGAGTAAACT 600
AGCAGATGGA GGACCTCTCT TTCTCTCTCT GCnTC 635

(2) INFORMATION FOR SEQ ID NO: 722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722:

ATCCTCTGCC TCTGTGAAGT TTAATATGTG TGGTTCCTCT TCTACGCACC AGACTGCATG 60
CTAGCTGCCA TCCACACAAT GTGCTCCCCC TGCCAACAGC CATAGGTCAT GTTCCAATGT 120
CAGCATTACT ACTGTTCACT TTAATATATC TAAATCTAA CATAAAAGTA TTTATAATGG 180
GCTGGCCCTG TGGCACAGCA GGTTAACGCA CAAGCCTGAA GCCCCAGTAT CCCATATGGG 240
CACCAGTTCT AGTCCTGGCT GCTCCTCTTC TGATCCAGCT ATCTGCTATG GCCTGGGAAG 300
GCAATAGAAG ATGGCCCAAG TACTTGGGCC CCTGCACCCA CATGGGAGAC CCGGAAGAGG 360
CTCCTGACTT CGGATCAGTG CAGTTCCAGC CATTGTGGCC ATCTAGGGAG TGAACCAGCA 420
GATGGAAGAC CTCTCTCTCT GTCTACCTCT CTCTGCAACT CTGTCTTTCA AATAAATCTT 480
TTAAAAAAA GTATTTGTAA CAATAATGGT GCTGTACCCA TGGCACCTAC TGTCTCCTTT 540
CAAGTCTGTA CTCTGTGAAA TGGAAGTAAC ACAGTTCAGA ACAGGTTTAT GGGCTACAGT 600
GTGACACCTT CATGCATGTA TATGATGTGT GCT 633

(2) INFORMATION FOR SEQ ID NO: 723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723:

TTCCCATTTT CATTTTGCT TAAGCACTAG ATATAACTAT TGTTATCATT TTCCAGATGA 60
AGAGGAACAG AGATTACCCA AGATGCTATT GCTAAGCATG ACAAAGTCAG CATTCAAACC 120
TGGAAGCATT TCTAATGAC GATGGTTAAT TTTTGTGTTGG ATTTGTCAGT CTAGTTGATT 180
GTATATACTA TATATATATA TATATATACT GTCTACAGAT TCCAAAAGGT TTTCTTTTAA 240

1132

AAAGATTTAT TTATTTGGCC GGCACGTGTG CTCACTAGGA TAATCCTCCA CCTTGGGGTG	300
ATGGCACACC GGGTTCTAGT CCTGGTCGGG GCGCCGGATT CTGTCCCGGT TGCCCTCTC	360
CCAGGCCTGC TCTCTGTTGT GTCCAGGGAG TGAGTGGTG GATGGCCCAA GTGCTTGGGC	420
CCTGCACCCC ATGGGAGACC AGGATAAGTA CCTTGCnCTT ACCATCG	467

(2) INFORMATION FOR SEQ ID NO: 724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724:

CGTACCCTAT TGTTTATTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA	60
CCCTGATAAA TGCTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATCAGCCT	120
TCTTTTCAGC TTCCTCCTTG GCGCCCGAGG CACAGnGAGC CGAGCATAGC CGCGCAGGCA	180
AGTGC	185

(2) INFORMATION FOR SEQ ID NO: 725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725:

CGGTACCTGG TCAGTTTGCA AACGGCCACG GTGGAGATGA GCGGCTTATA TTCCTCAGGA	60
GCGTGTGGCA GATTGTGGTG AAAGCGAATG GGTGTTGATA ACCGGGTTC GGGTAGAATT	120
CCCAGCCGCC TGGTGGCGAA GCCGCCCGGC GCCCCAAATT TTTCCCGGCG GTTnGCCCT	180
TACnGGTTC	189

(2) INFORMATION FOR SEQ ID NO: 726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726:

TAATTATGAA AACTGAATCA AGAAGACATA GAAAATCTGA ATACACTTAA AAAAAGAGGT	60
TGGATTAGTA ATTAAAAATT TCACACAAAG AAAAGTCTAG TCCCAGTTAT ATACTTTT	120
TAAAGATTTA TCTATTTATT CAAAAGTCAG AGTTACACGG AGAGAGGAGA GGCAGAGAGA	180
GGTCTTCCAT CCACTGGTTC ACTCCCCAGA TGGCCGCAAC GGCCAGAGCT GTACCGATCT	240
GAAGCCAGGA GCCAGGAGCC TTCTCTGGGT CTCCCATGTG GGTGCAGGGA CCCAAGGACT	300
TGGGCCATCT TGTACTGGTT TCCCAGACCA TAGCAGAGAG CTGGATTGGA AGAAGAGCAG	360
nTGGGACTCG AACCAGCCCC CATATGGGGT GCCGGCACTG CAGGCGGCGC TTAnCCGCT	420
ACGCCACAGA GG	432

(2) INFORMATION FOR SEQ ID NO: 727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727:

TCCTCCTGCA GCGCCAGTAT TCCATATGGA CACCAGTTCT TGTCTGGCAG TTCCACTGCC	60
AATCCAGCTC TCTGCTATGG CCTGGGAAAG CAGTGAAGA TCATCCAAGT CCTTGGGCCC	120
CTGAACCCAC GTGGGAGACC TACAAGAAGC TCCTGGCTTT GGATCAGCAC AGCTCCAGTC	180
GTTGCAGTCA TTTGGGGATT GAACCAAGTG ATGGAAGACC TCTCTGTCTT TACCTCTCTC	240
TGTCTGCAAC TCTGCCTCTC AAATGAATAA AATCTTTTAA AAATTTTAT TTATGTCTGT	300
ATTTTATTTG AAAGAGATGA GGAGGGAGAG AGCGTGAGAG CCAGTGCACA TGATACCTTT	360
CAACTGGTAG TTTACTGCCC TGTTGGCCTC AATGGCCAGG GCTAGGCCAG GCCAAAACCA	420
AGAGCTTC	428

(2) INFORMATION FOR SEQ ID NO: 728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728:

1134

TTTACTTGCT ATGTTACAG TTCCTACAGG AAAACTTGGA ACACAATAGA CATTCAAGCT 60
TTATTTGTTG AAGATTATGA ATATTTAGGA TGAGACACTG TGCTTTACGT TCCCCCCTA 120
AATCCCAAAG AAATGATATT ATTTGTGTAA TAAGTGACTT AAAACATATT TTCCTGAGGC 180
CAGTATTGTG GCATAGCAAC TAAAACTGCC ACCTGTGATG CCGACATCCC ATAGGGGTGC 240
CAGTTTGAGA CCCGGATGCT CCACTTCTGA TCCAGTCTCT TCCCTAATGC ACCTGGGAAA 300
GCAGTAGAGG ATGGCCCAAG TGCTTGGGCC CCTGTACCTA CGTGGAAGAC CCATAAGCTC 360
CTGGCTCCTG GCTTTGGCCT GGCCCAGCTC CAGCTGTTAC AGCCATCTGG GGAGTGAACC 420
AAAGGATGGA AGACCTCTCC ATGTCTCTCC CTCTCTCTGT GTA 463

(2) INFORMATION FOR SEQ ID NO: 729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729:

AACTCACGCA AAGAGAAATC GACAATATCA ACAGGTGTGT GTTTAAAAAA ATTGAATCCA 60
TAATTAAAC CTTCCAAAC AGAAAGCACA AGGCTCTGAT GACTTCAATC AAACATTCAA 120
TGAGGTATAG GAGCAGGTCT TTGGCCTAAT GGTAAAGATG TCCACGTCCC ATATTGGACT 180
GACTGGGTGT GATCCCTGGC TCTAGACTCA ATTTACAGCTT TCTGCTGATT TAGACCCTGG 240
GAGGCAGCAG GTCATCATTC AAATGGTTGG GTCACCTCCA CCCATGTGGG AGACATAGAT 300
AGAATTCCTG GCTCTTGTTT CTGGCCCTGG CCCAGCTAC CAGTCATTTT AAGCATATGA 360
AATGTGAATG AAAAATTAGA ATGTGTGATC TCAAATAAAT AAATACTTAA AAAAAAAAAA 420
AAACTAAATT ATCTAGGGCT GGCGCTGTGG CACAGTGGGT TAACGCCCTG GCCTGCAGCG 480
CCAGCATCCC ATATGGAAGC CGGTTCTAGT CCCAGCTGCT CCACTTCCAA TCCAGTTCCT 540
TGCTATGGCC TGGGATAGCA ATAGAAGATG GCCCAAGTCC TTG 583

(2) INFORMATION FOR SEQ ID NO: 730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730:

TTGGAGTTGT AATAAAAGGA ATTTTCCCTT CTACCTCCTT TCTGTAAGAA ACATCAGGCT	60
TTCTTGCCAC TGGTTAAACA TGATTAAGTG GTAAACAGTG ATGAATATTT CCCAGATAAC	120
TACATCTCAT GATGTTTTTT TAAAGATTTA TTTATTTATT TGAAAAGTAG AGTTAGAGAG	180
AGAGAGAGAG AGGCCTTCCG TCTGCTGGTT CACTCCCCAA ATGGCTGCAA TGGATGGAGC	240
TGGGCTGATC CAAAGCCAGG AGTCAGGAGC TTCTTCTGGG TCTTCCACAT GGGTGCTGGG	300
GCCCAAGGAC TTGTGCCATG TTCTACTGCT TTTCAAGGCC ATGGTAGAGA GCTGGATCAG	360
AAGTGAACA GCAGAGACTT GAATTGGTGT CCCTATGGGA TnCTGGCACT GnAGGCGATG	420
GCTTTACACA CAATGCCACA GTGCCAGTCC CTCATGATAT TTTTATTAAT GTTAATAGGn	480
TTCTGGTGGG CAAAAAATAG TTTGTAGAA AAATATTTTG GGAATACACT CAGATAACAT	540
TTGAGCAAGT TTCTTTCCTG CAGGACATAT CAGACAnTCA ACTATATTAn	590

(2) INFORMATION FOR SEQ ID NO: 731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731:

ATGCAAAAAT ATATACTAAA GGAAGTTTTT CAGGCAGAAG GAACATTGTA TCAGAAACTT	60
GAAGCTAAAC AAAGGCAGAG CACTAGAAAT GGAAAATAGT AAAATAAAAT TCATTTTTTC	120
ACAGTTTGAG TTGTTCTAAA AGATAACTGA CTTTCAGGGC CGGTGCTGTG GCACAGCAGG	180
TGGAGCTGCT GCCTTCAACA TGCCATCATC CCCTATGGGT GCCTGTTCAA ACCCTGGCTG	240
CCCCATTTCC TATTCAGCTC CTGCTGGTG TGCTGGGAG GGCAGCGGAA GATGGCCCAA	300
GTGCTTAGGC CCCTGCACCC ATGTGGGAGA CCCAGAGGAA GTTCTGGCT CCTGGCTTTG	360
GACTGGTCCA TCCCTGGCTG TTGTGGCCAT TTGGGGAATG AATCAGCAGA TGAAGATCT	420
CTCTTTCTCT GTCTGTCTGT CTGTCTCTCT CTGTAATGCT ACCTTTCAAA TAAAAAGTC	480
TATTTTAAAA AGATAACTGA TTTTCTAAAA TGGTAGAAAT GCATTATGTG TTTATAACAT	540
GTAAAAATAA AATGTATAAC AAATATAGCA CAATGGATTG GATAGAGGAA TTATGAAAAT	600
TCCTTTAACA TAGAATCATT ATATGTTACA TGAAATGTTG TAATATTATT TGAAGGnAGA	660
TTCTGATTAT ATATGCGTAA GGATAAACCC TAAGACAAC TCTAAAACAA	710

1136

(2) INFORMATION FOR SEQ ID NO: 732:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732:

TTTCACAGCA AATGCAACAA TTAGAAGAGA CACCTACAGA ATAGGAGAAA TTATTTACAA	60
ATCATAcata TAACATAGTG AGAATATCTG GAATATATGA AGAACTTAAT AGTAACCTAA	120
CCCCCAAAT AATTTGATTT AGAAATGGGC AAAGGTGGGG CCGGCGCTGT GGCTCAGTGG	180
GTTAACACCC TGGCCTGAAG TGCCAGCATC CCATATGGGC GTCCGTTCGA GACCCGGCTG	240
CTCCACTTCC AATCCAGCTC TTTGCTGTGG CTTGGGATAG CAGTAGAAGA TAGCCCAAGT	300
CCTTCGGCCC CTGCACCCGC ATGGGAGACC CAGAAGAAGC TCCTGGCTCC TGGCTTCGGA	360
TCAGAGCAGC TCCAGCCGTC ACGGCTAATT GGGGAGTGAA CCAGCAGATG GAAGATCTCG	420
ATCTCTCTCT CGATCTCTCT CTCTCTCTCT AACGCTGACT TTCAAATAAA TAAATAAATC	480
TTTTTTTTTAA AAAAATGGGG CAAAGGGCAT GAATAGACAC AGATATCCAA GAAGTATCTT	540
AAAAATGCTC AACATTACTA ATCATCAGAG AAATGCAAGT CAAAACCTCA TTGAGATATC	600
ACTTCACCCA GTTTTTTTTT T	621

(2) INFORMATION FOR SEQ ID NO: 733:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 606 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733:

TCAGAAATCA TATTTGAATT AAAATCTTTA AAATGGAGAA GCAACATCAT CTGAAGTATA	60
ATAATAACTA AGCATTTTAA ATTGTCAGAT ACAGGAAGCC ATAGAGGAGA ACAAGAGAAA	120
AAAAAAAAAAG GACTGAGGCC AATGATGTGA TGTAAGTGGG TAAGGCTCCA CCTGCAGTGC	180
CAGCATCCCA TATGGGTGCC GGTTCATGTC CCAGCTGCTC CTCTTCCAAT CCAGCTCTCT	240
GCTTATGGCC TGGGAAAGTG GCAGGAGATG GCCCAAGTGC TTGGGCCCCCT GTACTTGTGT	300
GGGAGACCCA TATGGATTTT CAGGCTCTTG GCTTTGGCCT GACCCAGCCC CAGCCATTGC	360

1137

AGCCATTGGA GGAGTGAACC AGTGGACGGA AGACCTCTCT CTGTCTGTCC CTCTGCCTGT 420
AGCTCTAACA TCTCAAATAA ATAAATAAAT CTTTAAAAAA GGAnGGGGGA GGAAGAGAAC 480
AAGAAGAAGA AAAAGAACTT ATGAAGAGGA AAGGGATGAA CCTATAGAGT ACTGGTAAAC 540
ACTGGGTTCA CATTTCAAAC CCAAGGCTGC CCATGGCAGT nAGCATTAC TCTAAAAGGG 600
AGCATG 606

(2) INFORMATION FOR SEQ ID NO: 734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734:

TGCTATGGCC TGGGAAAGCA GTAGAAGATG GCCCAAGTGT GTGGGCCCCCT GCACCTGTGT 60
GGGAGACCCA GAATAAGCTC TTGACTCCTG GCCAAGATTG GCGCAGTTCT GGCCACAGTG 120
GCCATCTGAG AAGTGAACCA GCGGATGGAA GACCTCTCTC TCTCTCTCTG CCTCTCCTCT 180
CTCCGTGTAA CTGTGACTTT CAAGTAAAT AAATACATAA AAAAAAAAAA AAAAGAAAGA 240
AAGAAAGAAA GAAAGTAAAC AGCTAGGTTG CTAGACACCA GAATCAGGAT GCACCATAGG 300
TTCTTACAT TGGAGAGTGG CATGGGGAAG TGATTGCTGG AGAAATGGTG AAGGnGACTA 360
TGAAACTTA ATCTAGAATA ACCTGTACCT TTTCCGAATT TACCATTCT TGTGAGATT 420
TAGGAGGnTA ATAACCAACA CCCCTTCCTC GnTCCCCCAA ATGTGG 466

(2) INFORMATION FOR SEQ ID NO: 735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735:

ATGCTACATG ATAATTTCAA GGGAGAAGCC AGTAGAGAAG AAACAAGAAG CCTAGAGATT 60
CTCCAAATGC ACAAAAATGC TGCCGTTCTT GAATTGCAAG CTGACTTGAA GCAGAGGAAT 120
GAGATTTCTT TTCCAAGTTA AAACAAATGC ACAGATTATC ATTGACTTCT TTCATTAAAA 180
GCATTTATTT TATTTATTTG AAAGAGTTAC ATAGAGAGGT AAAGTCAGAG AGAGAGAGAA 240

1138

AGAGGTCTTC CAACAGCTGG TTCACTCCCC AAATGACTGC AATGGCCAGT GCTGAGCTGA	300
TCCAAAGCCA GGAGCCAGAA TCTTCTTCTG GGTCTCCCAT GTGGATGCTG GGGCCCAAGG	360
ATTGCGGCCA TCTTCTGCTG CTTTCCCAGG ACATAGCAGA GAGCTGTATC GGAAGTGGAG	420
CAGCTGGGAC ACGAACTAGC ACCCACATGG GATGCCAGAA CTGCAGACCA AATCTTTAAT	480
CCATTGTGTC ACAGCACCAG CCTAGCATT AAGTTCCTTT TTTTCTTTT TTGACAGGCA	540
GAGTGGAAG TAAGAGTGAG AGTGAGA	567

(2) INFORMATION FOR SEQ ID NO: 736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736:

GAATTCTTC TGGCTTCTAG GGTGTGTGCC CAGGTCTTCC TCCTGAGGTT ACCTTCAGAT	60
GTTAGAATAG AAGTTGCAGG GCCAACGCTG AGGTGTGGCG GGTAAGAGCT GCCGCCTACA	120
GTGCCAGCAT CCCATATGGG CACTGGTTCG AGTCCCGGCT GCTCCACTTC CGATCCAGCT	180
CTCTGCTGTG GCCTGCGAAA GCATAGAAGA TGGCCCAAGT TCTTGGGTCT CTGCACCCAT	240
GTGGGAGACT CTGAAGTAGC TCCTAGCTCC TGGCTTCGGA GATCAGCACA GCTTTGGCGG	300
TTGCGGCTAA TTGGGAAGTG AACCATTGGA TGAAAGACCT CTCTCTCTTC nCTCTCTCTC	360
TGGCTTCTCC TTCTTTCTCT GTGTAACCTT TTCAAGTAAT AGTTAAATAA ACCTTAAAAA	420
AAAAAGAAT AGAAATTGCA TCTTTTCTA GTTAGAGCA GCCTGAGTCT CATTCCTCAC	480
AACTTTAAAG ATGGCTCTTC TCACCTGCAT AATGCATCAA GGTCTCCTCT TTTACTA	537

(2) INFORMATION FOR SEQ ID NO: 737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737:

TAACAAAGTG AAGAGGTAAT GAAACAATG AGAGAAAATA TTTGAAAAGT ATGCATCCAA	60
TAAAGGATTA ATATCAAGAA TATATAAGGA GTTCCAGAAA CTCAATAACA ACAAATAAT	120

1139

CCAGTTAAAA ATGTGCAAGG GCAGGAACAA GCATTTTTC AAGGATGAAA TAAAAAGGGC 180
CAACATGGGG CCAGCACTGT GGACATAGCA GGTAAAGCCA CCGCCTGCAA TACCAGTATT 240
CCATATGGGT GCTGGTTCAA GTCCCAGCTG CTCCACTTCT GATCTGGCTC TCTGCTATGG 300
CCCAGGAAAG CAGTAGAAGA TGGCCCAAGT CCTTGGGCCC CTGCACCCAC CTGGGAGACC 360
CAGAAGCTCC TGGCTCCTGG CTCTGGACTG GCTCAGCTCT GGCCATTGnC AGCCATTG 420
GGAGTGAACC ATTGGGTAGA AGCCCCCCCC TCTGTGTGTA ACTCTGACTT TGAAATAAAT 480
AAATAAATCT TAAAAA AAAAGCCAACA GACAGATGAA AAAACTCCAG GATGACTGCC 540
ATCAGGGAAA TGCAAATACA AATTACAGTG TGGTGTACC TTACCCAGC TAGAATGCTA 600
TCATTCAAAA ATCAAAAATG GA 622

(2) INFORMATION FOR SEQ ID NO: 738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738:

GAGCAAAGTG GCATTGAGAA GAAAAAATC GCCACATTTT GGACACTTTC CACAACCCTA 60
ACTATTCTTT TGGATTATGA TTTTGTTTTG TTTTGTTTTA AAGATTTTTT TATCTGTTTA 120
TTTCACAGGT AGAGTTAGTT ACAGACAGTG AGAGAGGGAG ACGGAAAGGT CTTCTTCCA 180
TTGGTTCACT CCCCAAATGG CCACCACAGC CAGAGCTACG CCGATCCGAA GCCAGGAGCC 240
AGGTGCTTGC TCCTGGTCTC CCATGTGGGC GCAGGGGCTC AAGCACTTGG GCCATCCTCC 300
ACTGCCCTCC CAGACCACAG CAGAAGGTGC TGGACTGGAA GAGGAGCAAC TGGGACTAGA 360
ACCTGGCACC CAACCTAATC ATTAATCCAT AAATACCTTA AATATATCCC CCTGGGGAAT 420
CTTGAGAGT TTATATACTA GAAAAAGCAT TTATTCATGA TTTAAATTT TTTTAAAGTT 480
TATAAAAACA TAACATAAAT CTTACCTTAA ATATCTGTAG nATGGGGTAn CTC 533

(2) INFORMATION FOR SEQ ID NO: 739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739:

TTTGTGCCA CAAATGCCCC TTCTCGGGG TGGCGCTGTG GCACAGTGGG TTAACGCCCT	60
GACCTGAGGC ATTAGCATCC CATGTGGGCA CTGGTTCAAG ACCCAGCTCT CTCCTGTGGC	120
CTGAGAAGGC AGTAGAAGAA AGCTCTAGTC TTTGGGCCCC TGCACCCATG TGGGAGACCC	180
AGAGGAGGCT CCTGGTTCCT GGCTTCGGAT CAGCACAGCT CCAGCCATCG CTGCTGGTTG	240
GGGAGTGAAC CATCAGATGG AGGACCATT CTTCTCTCTC TCTCTGCCTC TCCTCTCTCT	300
GTGTA ACTCT GACTTTCAGA TGAATAAATG AATCTTTAAA AAAAAATGCC CACTCTCTAC	360
ATAATGCTTT AAGATTCATC CATGATAGAG TACATGTGAT ATTTTGTTTA TTA CTGAATA	420
GTATTC AAG CATGTGTTT TGAAGGGACT AAATGAGCAG TTCTGGCCAA GGCTGGCTCA	480
CCTGGATCTT CCTTAGAGAC GAAATCCTAC AGCCCTC	517

(2) INFORMATION FOR SEQ ID NO: 740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740:

AGACCTTTCT CTCTGTCTCT CTTTCTCACT GTCCACTCTG CCTGTCAAAA AAAAAAAAAA	60
AAAAAAAAAA AAAGGAAAAA AAAGGAGAGG AAAGGATAAG GCCCCTGGGA GTGCTGTTCC	120
CTGGAATACA GTAAGGGGTG GCTGCTGGCT GCTCTCTGGG CTGTGGGCCT GGGTCAGCCC	180
AAGGTTCTTG GGGAGATACG CAGCTGGGGT TGTCAGAGTT AGCTCAGGAG AGAACTTACT	240
CCTCAAGCAC ACTTAGAGTG AACCTTTGCT AAGTTGGCTA CACAACTTCT CTATTCTGTA	300
AACCAGTTGA AATAAATCTT ATGGGTTTTG TTTGAAAGGA ATTTATATGA GCAATTTTAC	360
TAAATCAGGA ATATTTTAA AGATTGTTTA TTGGGGCCAG TGCTGTGGCA GCGGCTCCTC	420
TTCAATCCA GCTCCTGCTA ATTTGTCTGG GAAAGCAGTA GGAGATGGCC CAGGTGCTTG	480
GCCCCTTTAC TCACATGGGA GACCTGGAAG ACGCTCCTGG ATCCTGGCTT CAGCTCGGCT	540
CAGCTCTGGG nGTTGCAGCC ATCTGGGGAG TGAACCAACA GATGGAAGAC CTCTCCTTCT	600
CTCTGCCTCT GCCTCTATAA nTCTGCCTTT CAAATAAATA AAT	643

(2) INFORMATION FOR SEQ ID NO: 741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs

1141

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741:

TGCCAGTTCG AGTCCCGACT GCTCCACTTC TGACCCAGCT CTCTGCTATG GCGTGAGAAA	60
GCA GTGGAAG ATGGCCCAAG TCCTTTGGGC CCCTGCACTC CCATGGGAGA CCCAGAAGAA	120
GCTCTTTGCT CCTAGCTTTG GATCGGCTAG GAGCTCCAGC TGTTGCGACC AACTGGGGAG	180
TGAACCAGCA GTTGAAGATC TCTCTCTCTC TCGGCCTCTC CTTCTCTCTC TCTCTGTGTA	240
ACTCTGACTT TAAATAAAT AAGTAAATCT TCAAAACAAA AACAAAGTTT GGTTCCAATT	300
ATGATTACTT TGTTATTGCC AGTTTGTTGA TTAGGGTTCA CTTAAAACGA GATACTGTAA	360
ATCTGAGAAT ATACAGGGGC ACCTGGCGTC ACATCACAAA AAGTCTGGCA CATTTAGTT	420
TATTCAAGCA ACTATCCATG ATCTACATAG CTAAATGAAA CCTTATTCGT ATCTAAATAG	480
GCATCTGCCT CTAAATATTT TAATATGCAA TTCTGTCTCT ATTCTAATAA T	531

(2) INFORMATION FOR SEQ ID NO: 742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742:

AGGGAGTTTT TCCCTATGGT TGACCAAAG ATAATAAAC TACCTTGCTT ATTCAGACAG	60
AACGCAAAT CAGCATTCCT CTCTTCAACT GCTCAGCTGT AGGTCAATTG ATCCAACAG	120
TCCTATAAGT TAACATTTAA TATTTCCAGT GGATCTATTA AATTTTATTT GCGGAAGTGA	180
TTTCTTTTTA AGATATATAT GTATATATAA ATGCTTATTT TAAAAAATAT TTATTTGAAA	240
GGCAGGGTTA CATAGAGGCA GAATTAGAGA AGAGAGAGTG AGGTTTTCTA CCCATTGGTT	300
CACTTCCCAA ATGGCCACAA TGGCCGGAAC TGCGCCGATC TGAAGCCAGG AGCCAGGAGC	360
TTCTTCCAGG TCTCCACGT GATTGCAGGG ACCCAAGCAC TTGGATCATC TTCTGCTGCT	420
TTCTCAGGCC ACAGCAGAGA GCTGGATCAG AATTGGAGCA GCCAGGACTC AAAATGGTGC	480
CCATATAGGA TGCTGGCACT GCAGGCAATG GCTTTCCTCT GTATGTCACA GTGCTGGCCC	540
CAAAATGCTT GTTTTTATAT ATGTGTTTAT GTGTGTATTT TAAATTGGAGA GGCACAGAGG	600

1142

GAGAGAAAGC ATGCTACTAC CTGCAGGnTC ATT

633

(2) INFORMATION FOR SEQ ID NO: 743:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 681 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743:

TTATCATGTA ACACCACCCn TGCAGCCAAC TCAGGACCCC CCAACAAAGG TCACCACCAG	60
ATGCAACCCC TCGACCTGAG ACTTCTCTGT CTCCCAGAAT TATAAAAAA TATACATTTC	120
AGGGCAGGTG TTTGGCGCAG TGGGTATAGC TCTGACCTGT GATGTTGGCA CCCATATGGG	180
TGATGCTCCC TGTCCCAGCT GCTCTGTTTC CAATCCAGCT CCCTGATAAC GACCCAGGAA	240
AAGTAGCAGA AGTTGGCCCA AGTGTTTGGG TCTCTACCAC TTGTGCGGGA GACCTTAATG	300
AAGCCCCTGG CTTAGATCTG GCCCAGCTCT GGCCATTGCA GCCATCTGGG GAGTGAACCA	360
GTGGATGGAA GATGTCTCTG TTTCCATCTC TCCTTTTTTC TCTGCAACTC TTTCAAATAA	420
ATAAATAACA CACATTACTT AGCTTTGTGA ATTGCTTGAT CTCAGGTATT TGTTTTCTA	480
AGAGAGAACA GGTAAGATA TAGAGAGTGA AACCACCATA TGCAGTGCCG GTATCCTAAG	540
GGTGTGGGTT CGAGTCCCCG CTGTTCCACT TCCAATCCAG CTCCCTGCTG ATGCACCTGG	600
GAAAGCAGGG GAAGGTGGGC CAAGTGCTTG GGACCCTGAA CCCATGTGGG AGACCCAGAA	660
GAAGCTCCTG GCTCCCAACT T	681

(2) INFORMATION FOR SEQ ID NO: 744:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 651 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744:

TGGCCATCAA CATGGGGAAC TTGGATTGAA TTCTGTATT CTGATTTCAC TTTTACCCAG	60
TCGTAGTCAT TGTGGACAAT GCTGAATGAA CCATTGAGTG TGAATGTGTT ATAATAAAC	120
TGTATTTGAA AAAGGATTGA TTTTGTAGA CCAAAAATA AATAAAAATA AACAGAAAAG	180
ATTAAACACT TGATTTCTTC CTGAAAACAT GGTGAACACC TTAGAACTGG GATGCTCCAA	240

1143

TATGACTTGG AGTCTCAGAA TATAAATAAA GATACTTAGG AAGAAAAGTA GCCTTTATCA	300
CATTACTTTT TTTAAAAAAA TATTCATTTA TTTATTTGAA AATAAGAGTC AGACACACAC	360
ACACACACAC ACACACACAC ACACAAAGAT CTTTCATCTG TTGGTTCACT CCCCAAATGG	420
CCACAATAGC CAGAGCTGAG CCTATCTGAA GCCAGGAGCC AGGAACTTCA TCTGGGTCTC	480
CTACAnGGGT GCAGGAGCCC AAGGACTTGG GACATCTTCC ACTGCTATCC CAGGCCCGTC	540
TGCAGGGAGC TGGATCAGAA CTGGAACAGC TTGGGACATG AACTGGGCAC CCACATGGGn	600
TGCTGGGCAC TGCAGATGGT GACTAAACCT GCTGCATCAC AGTGCCTGCC C	651

What Is Claimed Is:

1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-744, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:.
2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-744 depicted in Tables 2 and 3 or a degenerate variant thereof.
3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *T. pallidum* genome of commercial importance comprising the following elements:
 - a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-744, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS: 1-744;
 - b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
 - c) retrieval means for obtaining said homologous sequence(s) of step (b).
6. A method for identifying commercially important nucleic acid fragments of the *T. pallidum* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS: 1-744, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS 1-744: with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
7. A method for identifying an expression modulating fragment of *T. pallidum* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS: 1-744, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS 1-744: with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.

8. An isolated protein-encoding nucleic acid fragment of the *T. pallidum* genome, wherein said fragment consists of the nucleotide sequence of any one of the fragments of SEQ ID NOS 1-744: depicted in Tables 2 and 3, or a degenerate variant thereof.

9. A vector comprising any one of the fragments of the *T. pallidum* genome SEQ ID NOS: 1-744 depicted in Tables 2 and 3 or a degenerate variant thereof.

10. An isolated fragment of the *T. pallidum* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a degenerate variant thereof.

11. A vector comprising any one of the fragments of the *T. pallidum* genome of claim 8.

12. An organism which has been altered to contain any one of the fragments of the *T. pallidum* genome of claim 8.

13. An organism which has been altered to contain any one of the fragments of the *T. pallidum* genome of claim 10.

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the fragments of the *T. pallidum* genome depicted in SEQ ID NOS: 1-744 and Tables 2 and 3 or a degenerate variant thereof.

15. An isolated nucleic acid molecule encoding a homolog of any of the fragments of the *T. pallidum* genome of SEQ ID NOS 1-744: and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising steps of:

- a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS: 1-744 and Tables 2 and 3, including fragments thereof;
- b) identifying members of said library which contain sequences that hybridize to said target sequence; and
- c) isolating the nucleic acid molecules from said members identified in step (b).

16. An isolated DNA molecule encoding a homolog of any one of the fragments of the *T. pallidum* genome of SEQ ID NOS: 1-744 and Tables 2 and 3, wherein said nucleic acid molecule is produced a process comprising steps of:

- a) isolating mRNA, DNA, or cDNA produced from an organism;
- b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *T. pallidum* genome to prime said amplification;
- c) isolating said amplified sequences produced in step (b).

17. An isolated polypeptide encoded by any of the fragments of the *T. pallidum* genome of SEQ ID NOS:1-744 and depicted in Table 2 and 3 or by a degenerate variant of said fragments.

18. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 17.

19. An antibody which selectively binds to any one of the polypeptides of claim 17.

20. A method for producing a polypeptide in a host cell comprising the steps of:

- a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of the *T. pallidum* genome of SEQ ID NOS: 1-744 and depicted in Tables 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and
- b) isolating said protein.

Figure 1

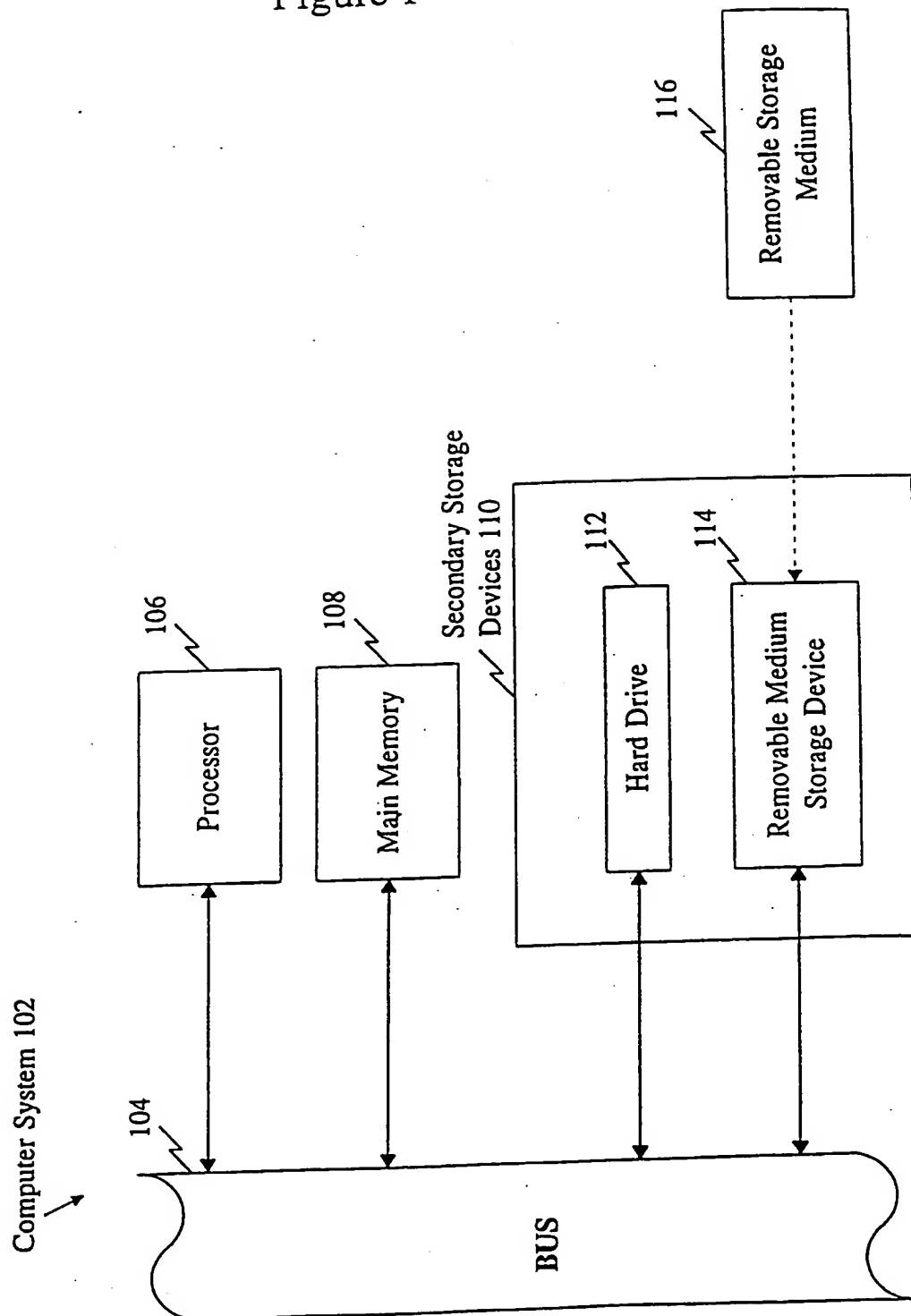


Figure 2

